

**FIGURE 1**

GTTACTGCACCCCAAAACAGGTCTGGCCACGGCCATGAGCATGCTGAGCCATCATGCCCAACCGTGGATGACATTCTG  
GAGCAGGTTGGGGAGTCTGGCTGGTTCCAGAAGCAAGCCTTCCTCATCTTATGCCTGCTGTGCGGTGCCTTTGCGCC  
CATCTGTGTGGGCATCGTCTTCCTGGGTTTCACACCTGACCACCACTGCCAGAGTCCTGGGGTGGCTGAGCTGAGCC  
AGCGCTGTGGCTGGAGCCCTGCGGAGGAGCTGAACTATACAGTGCCAGGCCTGGGGCCCGCGGGCGAGGCCTTCCTT  
GGCCAGTGCAGGCGCTATGAAGTGGACTGGAACCAGAGCGCCCTCAGCTGTGTAGACCCCTGGCTAGCCTGGCCAC  
CAACAGGAGCCACCTGCCGCTGGGTCCCTGCCAGGATGGCTGGGTGTATGACACGCCCGGCTCTTCCATCGTCACTG  
AGTTCAACCTGGTGTGTGCTGACTCCTGGAAGCTGGACCTCTTTCAGTCCTGTTTGAATGCGGGCTTCTTGTTTGGC  
TCTCTCGGTGTGGCTACTTTGCAGACAGGTTTGGCCGTAAGCTGTGTCTCCTGGGAAGTGTGCTGGTCAACGCGGT  
GTCGGGCGTGCTCATGGCCTTCTCGCCCAACTACATGTCCATGCTGCTCTTCCGCCTGCTGCAGGGCCTGGTCAGCA  
AGGGCAACTGGATGGCTGGCTACACCCTAATCACAGAATTTGTTGGCTCGGGCTCCAGAAGAACGGTGGCGATCATG  
TACCAGATGGCCTTACGGTGGGGCTGGTGGCGCTTACCGGGCTGGCCTACGCCCTGCCTCACTGGCGCTGGCTGCA  
GCTGGCAGTCTCCCTGCCACCTTCCTCTTCTGCTCTACTACTGGTGTGTGCCGGAGTCCCCTCGGTGGCTGTTAT  
CACAAAAAAGAAACACTGAAGCAATAAAGATAATGGACCACATCGCTCAAAGAATGGGAAGTTGCCTCCTGCTGAT  
TTAAAGATGCTTTCCTCGAAGAGGATGTCACCGAAAAGCTGAGCCCTTCATTTGCAGACCTGTTCCGCACGCCCGC  
CCTGAGGAAGCGCACCTTCATCCTGATGTACCTGTGGTTCACGGACTCTGTGCTCTATCAGGGGCTCATCCTGCACA  
TGGGCGCCACCAGCGGGAACCTCTACCTGGATTTCTTTACTCCGCTCTGGTCGAAATCCCGGGGGCCTTCATAGCC  
CTCATCACCATTGACCGCTGGGCCGCATCTACCCCATGGCCATGTCAAATTTGTTGGCGGGGGCAGCCTGCCTCGT  
CATGATTTTTATCTCACCTGACCTGCACTGGTTAAACATCATAATCATGTGTGTTGGCCGAATGGGAATCACCATTG  
CAATACAAATGATCTGCCTGGTGAATGCTGAGCTGTACCCACATTCGTCAGGAACCTCGGAGTGATGGTGTGTTCC  
TCCCTGTGTGACATAGGTGGGATAATCACCCCTTCATAGTCTTCAGGCTGAGGGAGGTCTGGCAAGCCTTGCCCT  
CATTTTGTTTGCGGTGTTGGGCCTGCTTGCCGCGGGAGTGACGCTACTTCTTCCAGAGACCAAGGGGGTCGCTTTGC  
CAGAGACCATGAAGGACGCCGAGAACCTTGGGAGAAAAGCAAAGCCCAAAGAAAACACGATTTACCTTAAGGTCCAA  
ACCTCAGAACCCCTCGGGCACCTTGAGAGAGATGTTTTGCGGCGATGTCTGTGTTGGAGGGATGAAGATGGAGTTATCCT  
CTGCAGAAATTCCTAGACGCCTTCACCTCTCTGTATTCTTCTCATACTTGCTACCCCAAATTAATATCAGTCCT  
AAAGAAAAAAAAAAAAAAAAAAAA

**FIGURE 2**

AATTAGCATAACCCTTCCTCAGGAAGAGTGAGATTTTATATTTGACAATAAAGTGTTAGACTCCATTTCTAAATACC  
AGACTTCAAAAGATAAGGTTCAAAAGTGTTATAAGAAGATATTCCTTTTTTTGTCCTAGAGAACTTATTTTCCTGTG  
AAAATGCCTACCACAAAGAAGACATTGATGTTCTTATCAAGCTTTTTCACCAGCCTGGGGTCCTTCATTGTAATTTT  
GCTCTATTCTTGGGACACAAGCATGGATCACCAGTACAATTGCTGTTAGAGACTCTGCTTCAAATGGGAGCATTTTC  
ATCACTTACGGACTTTTTTCGTGGGGAGAGTAGTGAAGAATTGAGTCACGGACTTGAGAACCAGAAAAAGTTTGC  
AGTTTTAGAGATACTGAATAATTCTTCCCAAAAACTCTGCATTCGGTGACTATCCTGTTCTGGTCCTGAGTTTGA  
TCACGTCGCTGCTGAGCTCTGGGTTTACCTTCTACAAACAGCATCAGCAACCCTTACCAGACATTCTGGGGCCCGA  
CGGGGGTGACACCTGGGAACGGGCTTCGGNGCATNCTTCGTTTTTGGTGACCATGATACTGGTTTGNNGGNAACAC  
GCAGGTCCCACCCAACCTTCCGAANAAGTTGTTCCAAAATGCTTTACCCCGGNAACCANCCAGTAAAGGAACGA  
CCCCACAGGTACCGGATACTCGTGCTGGCTCATACTGG

**FIGURE 3**

GATCAGTGTGTGAGGGAAGTCCATC**ATG**AGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCTGT  
 GTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCATTCT  
 AGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACAGGAAGC  
 CTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAGAAATGAAATATTTGTTGACCTAGCT  
 CTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTTGTTGAAATAAGAGGAAC  
 TTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCAACTACGATGTAA  
 TGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGACGTCCCTTTTGTGCTCACACTTAGA  
 ATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCTCCACTTTCCTATGTACCTGTGCCTATGAC  
 AGGACTAACAGACAGAATGACCTTCTGGAAAGAGTAAAAATTCATGCTTTTCAGTTTTGTTCCACTTCTGGATTC  
 AGGATTACGACTATCATTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCACTACATTATGTGAGACTGTG  
 GGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCCTCAACCATAACCAACCTAACTTTGAGTT  
 TGTGGAGGATTGCACCTGTAAACCTGCCAAAGCTTTGCCCTAAGGAAATGGAAAATTTTGTCCAGAGTTCCAGGGGAAG  
 ATGGTATTGTGGTGTCTTCTGCGGTCTGTTTCAAAATGTTACAGAAGAAAAGGCTAATATCATTGCTTCAGCC  
 CTTGCCCAGATCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAACCATCCACATTAGGAGCCAATACTCGGCT  
 GTATGATTGGATACCCACAGAATGATCTTCTTGGTCTATCCAAAACCAAAGCTTTTATCACTCATGGTGGAATGAATG  
 GGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTCCCATATTTGGTGATCAGCTTGATAACATAGCT  
 CACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAACTATGACAAGCGAAGATTTACTGAGGGCTTTGAG  
 AACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGAGATTATCAAGAATTCACCATGATCAACCTGTAAAGC  
 CCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTGATGCGCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCAT  
 GACCTCACCTGGTTCCAGCACTACTCTATAGATGTGATTGGGTTCTGCTGACCTGTGTGGCAACTGCTATATTTCTT  
 GTTCACAAAATGTTTTTTATTTTCCCTGTCAAAAATTTAATAAACTAGAAAAGATAGAAAAGAGGGGAAT**TAGAT**CTTTT  
 CAAATTCAGAAAGACCTGATGGGGTAATCCTGTTAATTCAGCCACATAGAATTTGGTGAAAACCTTGCTATTTTC  
 ATATTATCTATTCTGTTATTTTATCTTAGCTATATAGCCTAGAATTTCCATGATCATGAGGTTGTGAGTATATCTCAT  
 TCTTTCTGTTGATTTTCTTAGGTGTCTTTACTCTCTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATT  
 TTCCTATTTCTGATATGACTGTTTTGATGATGTCATTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGA  
 TTATTCCTGGTGTGCGCCCAAACACATGGATATAAGAGGTAAAAAATTTAAATTCACAAAATTCAGTAAACCACA  
 CAAATCAGGTAAGTGTTCTATGAGATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTCAATTTAAATAAGCC  
 TTTCTACATAGCCAGCATCAGTGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGT  
 TTGCTGTATTTCCATAGACCTCATCTAGATGTGATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGT  
 TTTCTTGATGATAAAAAGACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTTCTCACATAGAGA  
 ACATGTCAGTAAGATATTCAAGGTGAACAGATATTTTTGGGATTAGTAACCTATTTGAAATATGTGGTGATAATTACT  
 GAGTTTATAAAATTTATTTGATAGTACACTTAAAGAAGATTTATATGTTTATTCTTTAAAAATGATGAATACTCATA  
 ATTCTTATCTCTATAATCAAAAGTATAATTTACTGTAGAAAATAAAGAGATGCTTGTTCTGAAAGTAAGATCAGTG  
 AACTGCTTTTTCAGTCTCAATCTTTGAGAATTGTAAATTCATCAAATAATTGCTTACATAGTAAAAATTTAAGGTATT  
 AGAAAACCTGCATAACAAATAGTATTATATATTAAATATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTG  
 TAATAATGTTTACACTAGTAAGCAAATATGTTAATCTTCTCATTTTTTTACTGTATATAATCTTAGTGATATGCCT  
 ATTAATAGTTTTTAAATAAATAAATTGGCTTATCTGGCTTTTGGAAAATTTTGAAATTCCTACAGATGTTGATTAGGT  
 ATATCTACAAATTAATTTCAATTTTAAATGATGATATAAAAAATAAATAAGTATTTTTCTTGTGTATGTATACAA  
 TAAATATAAATAAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTTTA

**FIGURE 4**

GAGGATGCTGCTGGGGAAGATGTGCGCGCCGAGGTACCCGTCCGGGGGCGCCTGGGACCCTCACCAGGCCAGGCTT  
 CGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGGATGCTGGCCTCGGGCAGGCCCCCT  
 GGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATGTACTTCTGGGAGATGGGTTCCAAT  
 GCAGTTTCCTCAGCTCTTGGGGCCTGTTTGCTGCTCCGGGTGATGGCACGCCTGGAGCCTGACGCTGAGGAGGCAGC  
 ACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTGGCGAGTGCTATCGCAGCAGTGAGG  
 TGAGGGCTGCCCCGCTCCTCCTCCGTGCTGCCCCGCTCTGGGGGGGATGCCACTTGCCTCCAGCTGGCCATGCAAGC  
 TGACGCCCCGTGCCTTCTTTGCCCAGGATGGGGTACAGTCTCTGCTGACACAGAAGTGGTGGGGAGATATGGCCAGCA  
 CTACACCCATCTGGGGCCTGGTTCCTCGCCTTCTTTTGCCCTCCACTCATCTACACCCGCCTCATCACCTTCAGGAAA  
 TCAGAAGAGGAGCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATTAATGGGGAAGGGCCTGTGCGGAC  
 GGCGGACCCAGCCGAGAAGACGCCGTGGGGGTCCCGCGCCAGTCGGGCCGTCCGGGTGCTGCGGGGGCCGCTGCG  
 GGGGGCGCCGTGCCTACGCCGCTGGTTCACCTTCTGGGGCGCCGGTGACCATCTTCATGGGCAACGTGGTCAGC  
 TACCTGCTGTTCTGCTGCTTTTCTCGCGGGTGCTGCTCGTGATTTCCAGCCGGCGCCGCCCGGCTCCCTGGAGCT  
 GCTGCTCTATTTCTGGGCTTTACGCTGCTGTGCGAGGAACTGCGCCAGGGCCTGAGCGGAGGCGGGGGCAGCCTCG  
 CCAGCGGGGGCCCCGGGCCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAG  
 TGCGACCTAGTGGCTCTCACCTGCTTCTCCTGGGCGTGGGCTGCCGGCTGACCCCGGGTTTGTACCACCTGGGCCG  
 CACTGTCTCTGCATCGACTTCATGGTTTTACGGTGCGGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGC  
 CCAAGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCTCTTCTCCTCGGCGTGTGGCTGGTAGCC  
 TATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCG  
 TCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGT  
 CGGAGCCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGGCGGGCACCTGCGTCTCCCAGTATGCCAACTGGCTGGTG  
 GTGCTGCTCCTCGTCATCTTCTGCTCGTGCCAAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTCAAGTTACAC  
 ATTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGGTTACCGCCTCATCCGGGAATTCCACTCTCG  
 GCCCGCGCTGGCCCCGCCCTTTATCGTCATCTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGA  
 GCCCCAGCCGTCTCCCGGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGTGCTAACGT  
 GGAATCGGTGCATAAGGAGAACTTTCTGCTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAG  
 CGCACGTCCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCT  
 GGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCC  
 CAGGTGGGCCGCCACCCCTGACCTGCCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCCA  
 CAGGGGATTTTGCTCCTAGAGTAAGGCTCATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGCTCCTTGAGGTGAGC  
 CCCATGTCCATCTGGGCCACTGTGAGGACCACCTTTGGGAGTGTCATCCTTACAAACCACAGCATGCCCGGCTCCTC  
 CCAGAACCAGTCCCAGCCTGGGAGGATCAAGGCCTGGATCCCGGGCCGTATCCATCTGGAGGCTGCAGGGTCCCTTG  
 GGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCTTCACACTGGGGAAATAAAGCCATTTTCAGAGG

**FIGURE 5**

TNCCCGCAGAACCAGGAAAGTAACGGCTACAGACAGTGAGAAATAGTTTCGCTCGCCGGCTAGAAAACTCTGTCTGG  
TACCAACCCCAGAGCGTTGAGAGCAGCCCACCTCCACGCTTCCTTAACGGAGAGGTGCAGGACTCAGACTTCACCAG  
CCCCTCGGTCCCAGCCTTGTACGCAAAGAGACGCCAAGGACGCGCTCTCCCGCTCCAGGCAGCCCCAGCTTGCTG  
GCTTGCCCTGCCCGCTGCGTGCAGCACTCGGCCGGCGTGCAGCATGACCCTGTGGAACGGCGTACTGCCTTTTTTACC  
CCCAGCCCCGGCATGCCGCAGGCTTCAGCGTTCCACTGCTCATCGTTATTCTAGTGTTTTTGGCTCTAGCAGCAAGC  
TTCCTGCTCATCTTGCCGGGGATCCGTGGCCACTCGCGCTGGTTTTTGGTTGGTGAGAGTTCTTCTCAGTCTGTTTCAT  
AGGCGCAGAAATTGTGGCTGTGCACTTCAGTGCAGAATGGTTCGTGGGTACAGTGAACACCAACACATCCTACAAAG  
CCTTCAGCGCAGCGCGCGTTACAGCCCGTGTCTGGTCTGCTCGTGGGCCCTGGAGGGCATTAATATTACACTCACAGGG  
ACCCCACTGCATCAGCTGAACGAGACCATTGACTACAACGAGCAGTTCACCTGGCGTCTGAAAGAGAATTACGCCGC  
GGAGTACGCGAACGCACTGGAGAAGGGGCTGCCGGACCCAGTGCTCTACCTGGCGGAGAAGTTCACACCGAGTAGCC  
CTTGCGGCCTGTACCACCAGTACCACCTGGCGGGACACTACGCCTCGGCCACGCTATGGGTGGCGTTCTGCTTCTGG  
CTCCTCTCCAACGTGCTGCTCTCCACGCCGGCCCCGCTCTACGGAGGCCTGGCACTGCTGACCACCGGAGCCTTCGC  
GCTCTTCGGGGTCTTCGCCTTGCCCTCCATCTCTAGCGTGCCGCTCTGCCCCTCCGCCTAGGCTCCTCCGCGCTCA  
CCACTCAGTACGGCGCCGCCTTCTGGGTACGCTGGCAACCGGCGTCTGTGCCTCTTCCTCGGAGGGGGCCGTGGTG  
AGTCTCCAGTATGTTTCGGCCAGCGCTCTTCGCACCCTTCTGGACCAAAGCGCCAAGGACTGCAGCCAGGAGAGAGG  
GGGCTCACCTCTTATCCTCGGCGACCCACTGCACAAGCAGGCCGCTCTCCAGACTTAAAAATGTATCACCCTAACC  
TGTGAGGGGGACCCAATCTGGACTCCTTCCCCGCTTGGGACATCGCAGGCCGGGAAGCAGTGCCCGCCAGGCCCTGG  
GCCAGGAGAGCTCCAGGAAGGGCACTGAGCGCTGCTGGCGCGAGGCCTCGGACATCCGCAGGCACCAGGGAAAGTCT  
CCTGGGGCGATCTGTAAATAAACCTTTTTTTCTTTTGTTTTTTAAAAAAAATAAAAGTCGACC

**FIGURE 6**

CTGCAGGCTTCAGGAGGGGACACAAGC**CATG**GAGCGGCTTTGGGGTCTATTCCAGAGAGCGCAACAACCTGTCCCCAAG  
 ATCCTCTCAGACCGTCTACCAGCGTGTGGAAGGCCCGGAAAGGGCACCTGGAGGAGGAAGAGGAAGACGGGGAGG  
 AGGGGGCGGAGACATTGGCCCACTTCTGCCCCATGGAGCTGAGGGGCCCTGAGCCCCTGGGCTCTAGACCCAGGCAG  
 CCAAACCTCATTCCCTGGGCGGCAGCAGGACGGAGGGCTGCCCCCTACCTGGTCTTGACGGCCCTGCTGATCTTCAC  
 TGGGGCCTTCCTACTGGGCTACGTGCGCTTCCGAGGGTCTGCCAGGCGTGCGGAGACTCTGTGTTGGTGGTCAGTG  
 AGGATGTCAACTATGAGCCTGACCTGGATTTCACCCAGGGCAGACTCTACTGGAGCGACCTCCAGGCCATGTTCCCTG  
 CAGTTCCTGGGGGAGGGGCGCCTGGAGGACACCATCAGGCAAACCAGCCTTCGGGAACGGGTGGCAGGCTCGGCCGG  
 GATGGCCGCTCTGACTCAGGACATTGCGCGGGCGCTCTCCCGCCAGAAGCTGGACCACGTGTGGACCGACACGCACT  
 ACGTGGGGCTGCAATTCCCGGATCCGGCTCACCCCAACACCTGCACTGGGTGATGAGGCCGGGAAGGTTCGGAGAG  
 CAGCTGCCGCTGGAGGACCCTGACGTCTACTGCCCCACAGCGCCATCGGCAACGTACGGGAGAGCTGGTGTACGC  
 CCCTACGGGCGGCCCGAAGACCTGCAGGACCTGCGGGCCAGGGGCGTGATCCAGTGGGCCGCTGCTGCTGGTGC  
 GCGTGGGGGTGATCAGCTTCGCCCAGAAGGTGACCAATGCTCAGGACTTCGGGGCTCAAGGAGTGTCTATATACCCA  
 GAGCCAGCGGACTTCTCCCAGGACCCACCCAAGCCAAGCCTGTCCAGCCAGCAGGCAGTGTATGGACATGTGCACCT  
 GGGAACTGGAGACCCCTACACACCTGGCTTCCCTTCCTTCAATCAAACCCAGTTCCCTCCAGTTGCATCATCAGGCC  
 TTCCACAGCATCCCAGCCCAGCCCATCAGTGCAGACATTGCCTCCCGCCTGCTGAGGAAGCTCAAAGGCCCTGTGGCC  
 CCCAAGAATGGCAGGGGAGCCTCCTAGGCTCCCTTATCACCTGGGCCCCGGGCCACGACTGCGGCTAGTGGTCAA  
 CAATCACAGGACCTCCACCCCATCAACAACATCTTCGGGTGCATCGAAGGCCGCTCAGAGCCAGATCACTACGTTG  
 TCATCGGGGCCCAGAGGGATGCATGGGGCCCAGGAGCAGCTAAATCCGCTGTGGGGACGGCTATACTCCTGGAGCTG  
 GTGCGGACCTTTTCTCCATGGTGAGCAACGGCTTCCGGCCCCGAGAAGTCTCCTCTTCATCAGCTGGGACGGTGG  
 TGACTTTGGAAGCGTGGGCTCCACGGAGTGGCTAGAAGGCTACCTCAGCGTGTGACCTCAAAGCCGTAGTGTACG  
 TGAGCCTGGACAACGCAGTGTGGGGGATGACAAGTTTCATGCCAAGACCAGCCCCCTTCTGACAAGTCTCATTGAG  
 AGTGTCTGAAGCAGGTGGATTCTCCCAACCACAGTGGGCAGACTCTCTATGAACAGGTGGTGTTCACCAATCCCAG  
 CTGGGATGCTGAGGTGATCCGGCCCCTACCCATGGACAGCAGTGCCTATTCTTCACGGCCTTTGTGGGAGTCCCTG  
 CCGTCGAGTTCTCCTTTATGGAGGACGACCAGGCCTACCCATTCTGCACACAAAGGAGGACACTTATGAGAACCTG  
 CATAAGGTGCTGCAAGGCCGCTGCCCCCGTGGCCCCAGGCCGTGGCCAGCTCGCAGGGCAGCTCCTCATCCGGCT  
 CAGCCACGATCGCCTGCTGCCCCCTCGACTTCGGCCGCTACGGGGACGTCGTCTCAGGCACATCGGGAACCTCAACG  
 AGTTCTCTGGGGACCTCAAGGCCCGCGGGCTGACCCTGCAGTGGGTGTAAGTCTGGCGCGGGGGGACTACATCCGGCG  
 GCGGAAAAGCTGCGGCAGGAGATCTACAGCTCGGAGGAGAGAGACGAGCGACTGACACGCATGTACAACGTGCGCAT  
 AATGCGGGTGGAGTTCTACTTCTTTCCAGTACGTGTGCCAGCCGACTCCCCGTTCCGCCACATCTTCATGGGCC  
 GTGGAGACCACACGCTGGGCGCCCTGCTGGACCACCTGCGGCTGCTGCGCTCCAACAGCTCCGGGACCCCGGGGCC  
 ACCTCCTCCACTGGCTTCCAGGAGAGCCGTTTCCGGCGTCAGCTAGCCCTGCTCACCTGGACGCTGCAAGGGGCAGC  
 CAATGCGCTTAGCGGGGATGTCTGGAACATTGATAACAACCTTCT**TGA**GGCCCTGGGGATCCTCACATCCCCGTCCCC  
 AGTCAAGAGCTCCTCTGCTCCTCGCTTGAATGATTCAGGGTCAGGGAGGTGGCTCAGAGTCCACCTCTCATTGTCTGA  
 TCAATTTCTCATTACCCCTACACATCTCTCCACGGAGCCCAGACCCAGCACAGATATCCACACACCCCGACCCCTGC  
 AGTGTAGCTGACCCTAATGTGACGGTCATACTGTGCGTTAATCAGAGAGTAGCATCCCTTCAATCACAGCCCCTTCC  
 CCTTTCTGGGGTCTCCATACCTAGAGACCACTCTGGGAGGTTTGCTAGGCCCTGGGACCTGGCCAGCTCTGTTAGT  
 GGGAGAGATCGCTGGCACCATAGCCTTATGGCCAACAGGTGGTCTGTGGTGAAGGGGCGTGGAGTTTCAATATCAA  
 TAAACCACCTGATATCAATAAGCCAAAA

**FIGURE 7**

GCTGGAGCATCCCGCTCTGGTGCCGCTGCAGCCGGCAGAGATGGTTGAGCTCATGTTCCCGCTGTTGCTCCTCCTTC  
TGCCCTTCCTTCTGTATATGGCTGCGCCCCAAATCAGGAAAATGCTGTCCAGTGGGGTGTGTACATCAACTGTTTCAG  
CTTCCTGGGAAAGTAGTTGTGGTCACAGGAGCTAATACAGGTATCGGGAAGGAGACAGCCAAAGAGCTGGCTCAGAG  
AGGAGCTCGAGTATATTTAGCTTGCCGGGATGTGGAAGGGGAATTGGTGGCCAAAGAGATCCAGACCACGACAG  
GGAACCAGCAGGTGTTGGTGCGGAACTGGACCTGTCTGATACTAAGTCTATTCGAGCTTTGCTAAGGGCTTCTTA  
GCTGAGGAAAAGCACCTCCACGTTTTGATCAACAATGCAGGAGTGATGATGTGTCCGTACTCGAAGACAGCAGATGG  
CTTTGAGATGCACATAGGAGTCAACCACTTGGGTCACTTCCTCCTAACCCATCTGCTGCTAGAGAACTAAAGGAAT  
CAGCCCCATCAAGGATAGTAAATGTGTCTTCCCTCGCACATCACCTGGGAAGGATCCACTTCCATAACCTGCAGGGC  
GAGAAATTTACAATGCAGGCCTGGCCTACTGTACAGCAAGCTAGCCAACATCCTCTTCAACCAGGAAGTGGCCCG  
GAGACTAAAAGGCTCTGGCGTTACGACGTATTCTGTACACCCTGGCACAGTCCAATCTGAACTGGTTCGGCACTCAT  
CTTTCATGAGATGGATGTGGTGGCTTTTCTCCTTTTTCATCAAGACTCCTCAGCAGGGAGCCCAGACCAGCCTGCAC  
TGTGCCTTAACAGAAGGTCTTGAGATTCTAAGTGGGAATCATTTTCAGTGACTGTGATGTGGCATGGGTCTCTGCCCCA  
AGCTCGTAATGAGACTATAGCAAGGCGGCTGTGGGACGTCAGTTGTGACCTGCTGGGCCTCCCAATAGACTAAACAGG  
CAGTGCAGTTGGACCCAAGAGAAGACTGCAGCAGACTACACAGTACTTCTTGTCAAAATGATTCTCCTTCAAGGTTT  
TCAAAACCTTTAGCACAAAGAGAGCAAAACCTTCCAGCCTTGCCTGCTTGGTGTCCAGTTAAAACTCAGTGACTGC  
CAGATTTCGTCTAAATGTCTGTCTGTCATGTCCAGATTTACTTTGCTTCTGTTACTGCCAGAGTTACTAGAGATATCATAAT  
AGGATAAGAAGACCCCTCATATGACCTGCACAGCTCATTTTCTTCTGAAAGAACTACTACCTAGGAGAATCTAAGC  
TATAGCAGGGATGATTTATGCAAATTTGAACTAGCTTCTTTGTTTCAAAATTCAGTTTCTCCCAACCAACCAGTCTTC  
ACTTCAAGAGGGCCACACTGCAACCTCAGCTTAACATGAATAACAAAGACTGGCTCAGGAGCAGGGCTTGCCCAGGC  
ATGGTGGATCACCGGAGTCAGTAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCACCTCTACTAAAAATTGTG  
TATATCTTTGTGTGTCTTCTGTTTATGTGTGCCAAGGGAGTATTTTCAAAAGTTCAAAACAGCCACAATAATCAG  
AGATGGAGCAAACCAAGTCCATCCAGTCTTTATGCAAATGAAATGCTGCAAAGGGAAGCAGATTCTGTATATGTTGG  
TAACTACCCACCAAGAGCACATGGGTAGCAGGGAAGAAGTAAAAAAGAGAAGGAGAATACTGGAAGATAATGCACA  
AAATGAAGGGACTAGTTAAGGATTAAGTCCCTTTAAGGATTAAGTAAAGGATTAATAGCAAAAGACATTAAA  
TATGCTAACATAGCTATGGAGGAATTGAGGGCAAGCACCCAGGACTGATGAGGTCTTAACAAAAACCAGTGTGGCAAA

**FIGURE 8**

GCTCGGCCAGGCTGCTGGTACCTGCGTCCGCCCCGGCGAGCAGGACAGGCTGCTTTGGTTTGTGACCTCCAGGCAGGA  
CGGCCATCCTCTCCAGAAATGAAGATCTTCTTGCCAGTGCTGCTGGCTGCCCTTCTGGGTGTGGAGCGAGCCAGCTCG  
CTGATGTGCTTCTCCTGCTTGAACCAGAAGAGCAATCTGTACTGCCTGAAGCCGACCATCTGCTCCGACCAGGACAA  
CTACTGCGTGACTGTGTCTGCTAGTGCCGGCATTGGGAATCTCGTGACATTTGGCCACAGCCTGAGCAAGACCTGTT  
CCCCGGCCTGCCCCATCCCAGAAGGCGTCAATGTTGGTGTGGCTTCCATGGGCATCAGCTGCTGCCAGAGCTTTCTG  
TGCAATTTCAAGTGCGGCCGATGGCGGGCTGCGGGCAAGCGTCACCCTGCTGGGTGCCGGGCTGCTGCTGAGCCTGCT  
GCCGGCCCTGCTGCGGTTTGGCCCCTGACCGCCCAGACCCTGTCCCCGATCCCCAGCTCAGGAAGGAAAGCCCAG  
CCCTTTCTGGATCCCACAGTGTATGGGAGCCCCTGACTCCTCACGTGCCTGATCTGTGCCCTTGGTCCCAGGTCAGG  
CCCACCCCTGCACCTCCACCTGCCCCAGCCCCTGCCTCTGCCCCAAGTGGGGCCAGCTGCCCTCACTTCTGGGGTG  
GATGATGTGACCTTCCTTGGGGGACTGCGGAAGGGACGAGGGTTCCTGGAGTCTTACGGTCCAACATCAGGACCAA  
GTCCCATGGACATGCTGACAGGGTCCCCAGGGAGACCGTGTCAGTAGGGATGTGTGCCTGGCTGTGTACGTGGGTGT  
GCAGTGACAGTGAGAGCACGTGGCGGCTTCTGGGGGCCATGTTTGGGGAGGGAGGTGTGCCAGCAGCCTGGAGAGCC  
TCAGTCCCTGTAGCCCCCTGCCCTGGCACAGCTGCATGCACTTCAAGGGCAGCCTTTGGGGTTGGGGTTTCTGCCA  
CTTCCGGGTCTAGGCCCTGCCCCAAATCCAGCCAGTCTGCCCCAGCCCACCCACATTGGAGCCCTCCTGCTGCT  
TTGGTGCCTCAAATAAATACAGATGTCCCCAAAAAAAAAAAAAAAAAAAA



**FIGURE 9**

GAAGTTTCTCACTAGGGTCTTCTCTGGCCCAGCCTTTGACTGAAGCTGGTCTGGAGACAGGGGCATTAGAGAAGTGA  
CTCATAGATGGCCTAAAGAAGCGGGGCCACTCAAGGACCCAGGACAGAGGGAAGAGGGCCAACCCAGCTGGACCACA  
GGCAAACCCCATTTGCCTTTGAGAGAAAAGAAGAGGACCCGGTGAAACATGCTGCTGCTGAAGAAACACACGGAGGACA  
TCAGCAGCGTCTACGAGATCCGCGAGAGGCTCGGCTCGGGTGCCTTCTCCGAGGTGGTGTGGCCCAGGAGCGGGGC  
TCCGCACACCTCGTGGCCCTCAAGTGCATCCCCAAGAAGGCCCTCCGGGGCAAGGAGGCCCTGGTGGAGAACGAGAT  
CGCAGTGCTCCGTAGGATCAGTCACCCCAACATCGTCGCTCTGGAGGATGTCCACGAGAGCCCTTCCCACCTCTACC  
TGGCCATGGAACCTGGTGACGGGTGGCGAGCTGTTTGACCGCATCATGGAGCGCGGCTCCTACACAGAGAAGGATGCC  
AGCCATCTGGTGGGTGAGGTCTTGGCGCCGTCTCTACCTGCACAGCCTGGGGATCGTGCACCGGGACCTCAAGCC  
CGAAAACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGGACTCTCCAAAATCCAGG  
CTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGTGGCCCCAGAGCTCTTGGAGCAGAAACCTACGGG  
AAGGCCGTAGATGTGTGGGCCCTGGGCGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAG  
CGACCCTGAGCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTXTCCTTTCTGGGATGACATCTCAGAAT  
CAGGCAAAGACTTTATTTCGGCACCTTCTGGAGCGAGACCTTCAGAAGAGGTTACCTGCCAACAGGCCTTGCGGGAC  
CTTTGGATCTTTTGGGACACAGGCTTTGGCAGGGACATCTTAGGGTTTGTCAGTGAGCAGATCCGGAAGAACTTTGC  
TTGGACACACTGGAAGCGAGCCTTCAATGCCACCTTGTTTCCTGCGCCACATCCGGAAGCTGGGGCAGATCCCAGAGG  
GCGAGGGGGCCTCTGAGCAGGGCATGGSCCGXCACAGCCACTXAGGCCTTCGTGCTGGCCAGCCCCCAAGTGGTA  
TGCCCAGGXAGATGCCGAGGCCAAGTGGAAXTGAXCCCAGATTTXCTTXC

**FIGURE 10**

GGAACGAGTGGGAACGTAGCTGGTTCGCAGAGGGCACCAGCGGCTGCAGGACTTCACCAAGGGACCTGAGGCTCGTG  
 AGCAGGGACCCGCGGTGCGGGTTATGCTGGGGGCTCAGATCACCGTAGACAACCTGGACACTCAGGACCACGCC**ATGG**  
 AGGAGCTGCAGGATGATTATGAAGACATGATGGAGGAGAATCTGGAGCAGGAGGAATATGAAGACCCAGACATCCCC  
 GAGTCCCAGATGGAGGAGCCGGCAGCTCACGACACCGAGGCAACAGCCACAGACTACCACACCACATCACACCCGGG  
 TACCCACGAGGTCTATGTGGAGCTGCAGGAGCTGGTGATGGACGAAAAAGAACAGGAGCTGAGATGGATGGAGGCGG  
 CGCGCTGGGTGCAACTGGAGGAGAACCTGGGGGAGAATGGGGCCTGGGGCCCGCCGCACCTCTCTCACCTCACCTTC  
 TGGAGCCTCCTAGAGCTGCGTAGAGTCTTCACCAAGGGTACTGTCTCCTAGACCTGCAAGAGACCTCCCTGGCTGG  
 AGTGGCCAACCAACTGCTAGACAGGTTTATCTTTGAAGACCAGATCCGGCCTCAGGACCGAGAGGAGCTGCTCCGGG  
 CCCTGCTGCTTAAACACAGCCACGCTGGAGAGCTGGAGGCCCTGGGGGGTGTGAAGCCTGCAGTCTTGACACGCTCT  
 GGGGATCCTTCACAGCCTCTGCTCCCCAACACTCCTCACTGGAGACACAGCTCTTCTGTGAGCAGGGAGATGGGGG  
 CACAGAAGGGCACTCACCATCTGGAATTCTGGAAAAGATTCCCCCGGATTAGAGGCCACGTTGGTGCTAGTGGGCC  
 GCGCCGACTTCCTGGAGCAGCCGGTGTGGGCTTCGTGAGGCTGCAGGAGGCAGCGGAGCTGGAGGCGGTGGAGCTG  
 CCGGTGCCTATACGCTTCCTCTTTGTGTTGCTGGGACCTGAGGCCCCCCACATCGATTACACCCAGCTTGGCCGGGC  
 TGCTGCCACCCCTCATGTGAGAGGGGTGTTCCGCATAGATGCCTACATGGCTCAGAGCCGAGGGGAGCTGCTGCACT  
 CCCTAGAGGGCTTCCTGGACTGCAGCCTAGTGCTGCCTCCACCGATGCCCCCTCCGAGCAGGCACTGCTCAGTCTG  
 GTGCCTGTGAGAGGGAGCTACTTCGAAGGCGCTATCAGTCCAGCCCTGCCAAGCCAGACTCCAGCTTCTACAAGGG  
 CCTAGACTTAAATGGGGGCCAGATGACCCCTCTGCAGCAGACAGGCCAGCTCTTCGGGGGCTGGTGCGTGATATCC  
 GCGCCGCTACCCCTATTACCTGAGTGACATCACAGATGCATTACAGCCCCAGGTCTGGCTGCCGTCATCTTCATC  
 TACTTTGCTGCACTGTACCCGCCATCACCTTCGGCGGCCCTCCTGGGAGAAAAGACCCGGAACAGATGGGAGTGTC  
 GGAGCTGCTGATCTCCACTGCAGTGCAGGGCATTCTCTTCGCCCTGCTGGGGGCTCAGCCCCCTGCTTGTGGTCCGGCT  
 TCTCAGGACCCCTGCTGGTGTTTGAAGGAGCCTTCTTCTCGTTCTGCGAGACCAACGGTCTAGAGTACATCGTGGGC  
 CGCGTGTGGATCGGCTTCCTGGCTCATCTGCTGGTGGTGTTGGTGGTGGCCTTCGAGGGTAGCTTCTGGTCCGCTT  
 CATCTCCCGCTATACCCAGGAGATCTTCTCCTTCCTCATTTCCCTCATCTTCATCTATGAGACTTTCTCCAAGCTGA  
 TCAAGATCTTCCAGGACCACCCACTACAGAAGACTTATAACTACAACGTGTTGATGGTGCCCAAACCTCAGGGCCCC  
 CTGCCCCAACACAGCCCTCCTCTCCCTTGTGCTCATGGCCGGTACCTTCTTCTTTGCCATGATGCTGCGCAAGTTCAA  
 GAACAGCTCCTATTTCCCTGGCAAGCTGCGTCGGGTATCGGGGACTTCGGGGTCCCCATCTCCATCCTGATCATGG  
 TCCTGGTGGATTTCTTCATTCAGGATACCTACACCCAGAACTCTCGGTGCCTGATGGCTTCAAGGTGTCCAACCTCC  
 TCAGCCCCGGGCTGGGTTCATCCACCCACTGGGCTTGCGTTCCGAGTTTCCCATCTGGATGATGTTTGCCTCCGCCCT  
 GCCTGCTCTGCTGGTCTTCATCCTCATATTCTGGAGTCTCAGATCACACGCTGATTGTGAGCAAACTGAGCGCA  
 AGATGGTCAAGGGCTCCGGCTTCCACCTGGACCTGCTGCTGGTAGTAGGCATGGGTGGGGTGGCCGCCCTCTTTGGG  
 ATGCCCTGGCTCAGTGCCACCACCGTGCGTCCGTCACCCATGCCAAGCCCTCACTGTGATGGGCAAAGCCAGCAC  
 CCCAGGGGCTGCAGCCCAGATCCAGGAGGTCAAAGAGCAGCGGATCAGTGGACTCCTGGTCGCTGTGCTTGTGGGCC  
 TGTCCATCCTCATGGAGCCCATCCTGTCCCGCATCCCCCTGGCTGTACTGTTGGCATCTTCTCTACATGGGGGTC  
 ACGTCGCTCAGCGGCATCCAGCTCTTTGACCGCATCTTGCTTCTGTTCAAGCCACCCAAGTATCACCCAGATGTGCC  
 CTACGTCAAGCGGTGAAGACCTGGCGCATGCACTTATTACGGGCATCCAGATCATCTGCCTGGCAGTGCTGTGGG  
 TGGTGAAGTCCACGCCGGCCTCCCTGGCCCTGCCCTTCGTCCTCATCTCACTGTGCCGCTGCGGCGCGTCTGCTG  
 CCGCTCATCTTCAGGAACGTGGAGCTTCAGTGTCTGGATGCTGATGATGCCAAGGCAACCTTTGATGAGGAGGAAGG  
 TCGGGATGAATACGACGAAGTGGCCATGCCTGTG**TGAG**GGGGCGGGCCCAGGCCCTAGACCCTCCCCACCATTCCAC  
 ATCCCCACCTTCCAAGGAAAAGCAGAAGTTCATGGGCACCTCATGGACTCCAGGATCCTCCTGGAGCAGCAGCTGAG  
 GCCCCAGGGCTGTGGGTGGGGAAGGAAGGCGTGTCAGGAGACCTTCCACAAAGGGTAGCCTGGCTTTTCTGGCTGG  
 GGATGGCCGATGGGGCCACATTAGGGGGTTTGTGTCACAGTCCCTCCTGTTGCCACACTTCACTGGGGATCCCGT  
 GCTGGAAGACTTAGATCTGAGCCCTCCCTCTTCCAGCACAGGCAGGGGTAGAAGCAAAGGCAGGAGGTGGGTGAGC  
 GGGTGGGGTGTGCTGTGTGACCTTGGGCAAGTCCCTTGACCTTTCCAGCCTATATTTCTCTCTGTAAAATGGG  
 TATATTGATGATAATACCCACATTACAGGATGGTTACTGAGGACCAAAGATACATGTAAAATAGGGCTTTGTAAACT  
 CCACAGGGACTGTTCTATAGCAGTCATCATTTGTCTTTGAACGTACCAAGGTCACATAGCTGGGATTTGAACTGAG  
 CCGTGCAGCT

**FIGURE 11**

CTCTTTTGCTNGGACTTCACTGTCACTCANGAAAAAGCNGTGAANCTAAAACAGAAGAATCTTAGCACTGAGATAAG  
 GGAGAACCTGTCAGAGCTCCGTCAGGAGAATTCCAAGTTGACGTTCAATCAGCTGCTGACCCGCTTCTCTGCCTACA  
TCGCTAGCCTGGGTTGTCTCTACAGGAGTGGCCATAGCCTGCTGTGCAGCCGTTTATTACCTGGCTGAGTACAACCTTA  
 GAGTTCCTGAAGACACACAGTAACCTGGGGCGGTGCTGTTACTGCCTTTCGTTGTGTCTGCATTAATCTGGCCGT  
 GCCATGCATCTACTCCATGTTCAAGCTTGTGGAGAGGTACGAGATGCCACGGCACGAAGTCTACGTTCTCCTGATCC  
 GAAACATCTTTTTGAAAATATCAATCATTGGCATTCTTTGTTACTATTGGCTCAACACCGTGGCCCTGTCTGGTGAA  
 GAGTGTGGGAAACCTCATTTGGCCAGGACATCTACCGGCTCCTTCTGATGGATTTTGTGTTCTCTTTAGTCAATTC  
 CTTCTGGGGGAGTTTCTGAGGAGAATCATTGGGATGCAACTGATCACAAGTCTTGGCCTTCAGGAGTTTGACATTG  
 CCAGGAACGTTCTAGAACTGATCTATGCACAACTCTGGTGTGGATTGGCATCTTCTTCTGCCCCCTGTGCCCTTT  
 ATCCAAATGATTATGCTTTTCATCATGTTCTACTCCAAAAATATCAGCCTGATGATGAATTTCCAGCCTCCGAGCAA  
 AGCCTGGCGGGCCTCACAGATGATGACTTTCTTCATCTTCTTGCTCTTTTTCCCATCCTTCACCGGGGTCTTGTGCA  
 CCCTGGCCATCACCATCTGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTTCGAGGTCTGCCTCTCTTCATTAC  
 TCCATCTACAGCTGGATCGACACCCTAAGTACACGGCTGGCTACCTGTGGGTGTTTGGATCTATCGGAACCTCAT  
 TGGAAGTGTGCACTTCTTTTTCATCCTCACCTCATTGTGCTAATCATCACCTATCTTTACTGGCAGATCACAGAGG  
 GAAGGAAGATTATGATAAGGCTGCTCCATGAGCAGATCATTAATGAGGGCAAAGATAAAATGTTCCCTGATAGAAAAA  
 TTGATCAAGCTGCAGGATATGGAGAAGAAAGCAAACCCAGCTCACTTGTTCTGGAAAGGAGAGAGGTGGAGCAACA  
 AGGCTTTTTGCATTTGGGGGAACATGATGGCAGTCTTGACTTGCGATCTAGAAGATCAGTTCAAGAAGGTAATCCAA  
 GGGCCTGATGACTCTTTTGGTAACCAGACACCAATCAAATAAGGGGAGGAGATGAAAATGGAATGATTTCTTCCATG  
 CCACCTGTGCCTTTAGGAACTGCCCAGAAGAAAATCCAAGGCTTTAGCCAGGAGCGGAAACTGACTACCATGTAATT  
 ATCAAAGTAAAATTGGGCATTCCATGCTATTTTAAATACCTGGATTGCTGATTTTTCAAGACAAAATACTTGGGGTT  
 TTCCAATAAAGATTGTTGTAATATTGAAATGAGCCTACAAAAACCTAGGAAGAGATAACTAGGGAATAATGTATATT  
 ATCTTCAAGAAATGTGTGCAGGAATGATTGGTTCTTAGAAATCTCTCCTGCCAGACTTCCCAGACCTGGCAAAGGTT  
 TAGAAACTGTTGCTAAGAAAAGTGGTCCATCCTGAATAAACATGTAATACTCCAGCAGGGATATGAAGCCTCTGAAT  
 TGTAGAACCTGCATTTATTTGTGACTTTGAACTAAAGACATCCCCCATGTCCCAAAGGTGGAATACAACCAGAGGTC  
 TCATCTCTGAACCTTCTTGCCTACTGATTACATGAGTCTTTGGAGTCGGGGATGGAGGAGGTTCTGCCCCCTGTGAGG  
 TGTTATACATGACCATCAAAGTCCTACGTCAAGCTAGCTTTGCACAGTGGCAGTACCGTAGCCAATGAGATTTATCC  
 GAGACGCGATTATTGCTAATTGGAAATTTTCCCAATACCCACCGTGATGACTTGAAATATAATCAGCGCTGGCAAT  
 TTTTGACAGTCTCTACGGAGACTGAATAAGAAAAAAGAAAAAGAAATAGCTGGGTGCGATGGCTTATGCCTG  
 TAATCCCGGCACCTTTGGGAGGCTGAGGCAAGCGGATCACTTAATGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG  
 TGAACCCCGTCTCTACTAAGGATAAAAAAACTGGCTGGGCGTGGTGGTACATGCCT

**FIGURE 12**

GCTTCAGGGTACAGCTCCCCCGCAGCCAGAAGCCGGGCCTGCAGCCCCTCAGCACCGCTCCGGGACACCCACCCGC  
TTCCCAGGCGTGACCTGTCAACAGCAACTTCGCGGTGTGGTGAACCTCTCTGAGGAAAAACCATTTTGATTATTACTC  
TCAGACGTGCGTGGCAACAAGTGAAGTGAAGCTGAGACCTAGAAATCCAAGCGTTGGAGGTCCTGAGGCCAGCCTAAGTCGCTT  
CAAAATGGAACGAAGGCGTTTGTGGGGTTCCATTTCAGAGCCGATACATCAGCATGAGTGTGTGGACAAGCCACGGA  
GACTTGTGGAGCTGGCAGGGCAGAGCCTGCTGAAGGATGAGGCCCTGGCCATTGCCGCCCTGGAGTTGCTGCCCAGG  
GAGCTCTTCCCGCCACTCTTCATGGCAGCCTTTGACGGGAGACACAGCCAGACCCTGAAGGCAATGGTGCAGGCCTG  
GCCCTTCACCTGCCTCCCTCTGGGAGTGCTGATGAAGGGACAACATCTTCACCTGGAGACCTTCAAAGCTGTGCTTG  
ATGGACTTGATGTGCTCCTTGCCCAGGAGGTTGCCCCAGGAGGTGGAAACTTCAAGTGTGGATTTACGGAAGAAC  
TCTCATCAGGACTTCTGGACTGTATGGTCTGGAAACAGGGCCAGTCTGTACTCATTTCAGAGCCAGAAGCAGCTCA  
GCCCATGACAAAGAAGCGAAAAGTAGATGGTTTGAGCACAGAGGCAGAGCAGCCCTTCATTCCAGTAGAGGTGCTCG  
TAGACCTGTTCCCTCAAGGAAGGTGCCTGTGATGAATTGTTCTCCTACCTCATTCAGAAAGTGAAGCGAAAGAAAAAT  
GTACTACGCCTGTGCTGTAAGAAGCTGAAGATTTTTTGCAATGCCCATGCAGGATATCAAGATGATCCTGAAAATGGT  
GCAGCTGGACTCTATTGAAGATTTGGAAGTGAAGTGTACCTGGAAGCTACCCACCTTGGCGAAATTTCTCCTTACC  
TGGGCCAGATGATTAATCTGCGTAGACTCCTCCTCTCCACATCCATGCATCTTCCTACATTTCCCCGGAGAAGGAA  
GAGCAGTATATCGCCAGTTACCTCTCAGTTCTCAGTCTGCAGTGCCTGCAGGCTCTCTATGTGGACTCTTTATT  
TTTCCTTAGAGGCCGCTGGATCAGTTGCTCAGGCACGTGATGAACCCCTTGGAACCCCTCTCAATAACTAACTGCC  
GGCTTTTCGGAAGGGGATGTGATGCATCTGTCCAGAGTCCCAGCGTCAGTCAGCTAAGTGTCTGAGTCTAAGTGGG  
GTCATGCTGACCGATGTAAGTCCCGAGCCCCTCCAAGCTCTGCTGGAGAGAGCCTCTGCCACCCTCCAGGACCTGGT  
CTTTGATGAGTGTGGGATCACGGATGATCAGCTCCTTGCCCTCCTGCCTTCCCTGAGCCACTGCTCCAGCTTACAA  
CCTTAAGCTTCTACGGGAATTCATCTCCATATCTGCCTTGACAGTCTCCTGCAGCACCTCATCGGGCTGAGCAAT  
CTGACCCACGTGCTGTATCCTGTCCCCCTGGAGAGTTATGAGGACATCCATGGTACCCTCCACCTGGAGAGGCTTGC  
CTATCTGCATGCCAGGCTCAGGGAGTTGCTGTGTGAGTTGGGGCGGCCAGCATGGTCTGGCTTAGTGCCAACCCCT  
GTCCTCACTGTGGGACAGAACCTTCTATGACCCGGAGCCCATCCTGTGCCCCGTGTTTCATGCCTAACTAGCTGGGT  
GCACATATCAAATGCTTCATTCTGCATACTTGACACTAAAGCCAGGATGTGCATGCATCTTGAAGCAACAAAGCAG  
CCACAGTTTCAGACAAATGTTCAAGTGTGAGTGAGGAAAACATGTTCAAGTGAAGGAAAAACATTCAGACAAATGTTCA  
GTGAGGAAAAAAGGGGAAGTTGGGGATAGGCAGATGTTGACTTGAGGAGTTAATGTGATCTTTGGGGAGATACATC  
TTATAGAGTTAGAAATAGAATCTGAATTTCTAAAGGGAGATTCTGGCTTGGAAGTACATGTAGGAGTTAATCCCTG  
TGTAGACTGTTGTAAAGAACTGTTGAAAATAAAGAGAAGCAATGTGAAGCAAAAAAAAAAAAAAAAAA

**FIGURE 13**

GGGCAGGCTCAGTGTGAGTGAAGTGGAGGCTTCTCTACAACATGACCCAAAGGAGCATTGCAGGTCCTATTTGCAAC  
CTGAAGTTTGTGACTCTCCTGGTTGCCTTAAGTTCAGAACTCCCATTCTGGGAGCTGGAGTACAGCTTCAAGACAA  
TGGGTATAATGGATTGCTCATTGCCATTAATCCTCAGGTACCTGAGAATCAGAACCTCATCTCAAACATTAAGGAAA  
TGATAACTGAAGCTTCATTTTACCTATTTAATGCTACCAAGAGAAGAGTATTTTTTCAGAAATATAAAGATTTTAATA  
CCTGCCACATGGAAAGCTAATAATAACAGCAAAATAAAACAAGAATCATATGAAAAGGCAAATGTCATAGTGACTGA  
CTGGTATGGGGCACATGGAGATGATCCATACACCCCTACAATACAGAGGGTGTGGAAAAGAGGGAAAATACATTCAAT  
TCACACCTAATTTCTACTGAATGATACTTAACAGCTGGCTACGGATCACGAGGCCGAGTGTGTGTCATGAATGG  
GCCCACCTCCGTTGGGGTGTGTTTCGATGAGTATATCAATGACAAACCTTTCTACATAAATGGGCAAAATCAAATTAA  
AGTGACAAGGTGTTTCATCTGACATCACAGGCATTTTTGTGTGTGAAAAAGGTCTTGCCCCAAGAAAACCTGTATTA  
TTAGTAAGCTTTTTAAAGAAGGATGCACCTTTATCTACAATAGCACCCAAAATGCAACTGCATCAATAATGTTTCATG  
CAAAGTTTATCTTCTGTGGTTGAATTTTGTAAATGCAAGTACCCACAACCAAGAAGCACCAAACCTACAGAACCAGAT  
GTGCAGCCTCAGAAGTGCATGGGATGTAATCACAGACTCTGCTGACTTTACCACAGCTTTCCCATGAATGGGACTG  
AGCTTCCACCTCCTCCCACATTCTCGCTTGTACAGGCTGGCGACAAAGTGGTCTGTTTGTGCTGGATGTGTCCAGC  
AAGATGGCAGAGGCTGACAGACTCCTTCAACTACAACAAGCCGAGAAATTTTATTTGATGCAGATTGTTGAAATTCA  
TACCTTCGTGGGCATTGCCAGTTTCGACAGCAAAAGGAGAGATCAGAGCCCAGCTACACCAAATTAACAGCAATGATG  
ATCGAAAGTTGCTGGTTTTCATATCTGCCCACTGTATCAGCTAAAACAGACATCAGCATTTGTTTCAGGGCTTAAG  
AAAGGATTTGAGGTGGTTGAAAACTGAATGGAAAAGCTTATGGCTCTGTGATGATATTAGTGACGAGCGGAGATGA  
TAAGCTTCTTGGCAATTGCTTACCCACTGTGCTCAGCAGTGGTTCAACAATTCACCTTGCCTGGGTTTCATCTG  
CAGCCCCAAATCTGGAGGAATTATCACGTCTTACAGGAGGTTTAAAGTTCTTTGTTCCAGATATATCAAACCTCCAAT  
AGCATGATTGATGCTTTTCAGTAGAATTTCTCTGGAACCTGGAGACATTTTCCAGCAACATATTCAGCTTGAAAGTAC  
AGGTGAAAATGTCAAACCTCACCATCAATTGAAAAACACAGTGACTGTGGATAATACCTGTGGGCAACGACACTATGT  
TTCTAGTTACGTGGCAGGCCAGTGGTCTCTGAGATTATATTATTTGATCCTGATGGACGAAAATACTACACAAAT  
AATTTTATCACCAATCTAATTTTTCGGACAGCTAGTCTTTGGATTCCAGGAACAGCTAAGCCTGGGCACTGGACTTA  
CACCTTGAACAATACCCATCATTTCTCTGCAAGCCCTGAAAGTGACAGTGACCTCTCGCGCCTCCAACCTCAGCTGTGC  
CCCCAGCCACTGTGGAAGCCTTTGTGGAAAGAGACAGCCTCCATTTTCTCATCTGTGATGATTTATGCCAATGTG  
AAACAGGGATTTTATCCCATTTCTTAATGCCACTGTCTGTCACAGTTGAGCCAGAGACTGGAGATCCTGTTACGCT  
GAGACTCCTTGATGATGGAGCAGGTGCTGATGTTATAAAAAATGATGGAATTTACTCGAGGTATTTTTTCTCCTTTG  
CTGCAAATGGTAGATATAGCTTGAAAGTGCAATGCAATCACTCTCCAGCATAAGCACCCAGCCCACTCTATTCCA  
GGGAGTCATGCTATGTATGTACCAGGTACACAGCAAAACGGTAATATTTCAGATGAATGCTCCAAGGAAATCAGTAGG  
CAGAAATGAGGAGGAGCGAAAGTGGGGCTTTAGCCGAGTCAGCTCAGGAGGCTCCTTTTCAGTGCTGGGAGTTCCAG  
CTGGCCCCCACCCTGATGTGTTTCCACCATGCAAAATATTGACCTGGAAGCTGTAAAAGTAGAAGAGGAATTGACC  
CTATCTTGGACAGCACCTGGAGAAGACTTTGATCAGGGCCAGGCTACAAGCTATGAAATAAGAATGAGTAAAAGTCT  
ACAGAATATCCAAGATGACTTTAACAATGCTATTTTAGTAAATACATCAAAGCGAAATCCTCAGCAAGCTGGCATCA  
GGGAGATATTTACGTTCTCACCCCAAATTTCCACGAATGGACCTGAACATCAGCCAAATGGAGAAAACACATGAAAGC  
CACAGAATTTATGTTGCAATACGAGCAATGGATAGGAACTCCTTACAGTCTGCTGTATCTAACATTGCCAGGCGCC  
TCTGTTTATTTCCCCCAATTCTGATCCTGTACCTGCCAGAGATTATCTTATATTGAAAGGAGTTTAAACAGCAATGG  
GTTTGATAGGAATCATTTGCCTTATTATAGTTGTGACACATCATACTTTAAGCAGGAAAAAGAGAGCAGACAAGAAA  
GAGAATGGAACAAAATTATTATAAATAAATATCCAAAGTGTCTTCTTCTTAGATATAAGACCCATGGCCTTCGACT  
ACAAAAACATACTAACAAGTCAAATTAACATCAAACTGTATTAAATGCATTGAGTTTTTGTACAATACAGATAA  
GATTTTTTACATGGTAGATCAACAATTTCTTTTGGGGGTAGATTAGAAAACCTTACACTTTGGCTATGAACAAATAA  
TAAAAATATTCTTTAAAGTAATGTCTTTAAAGGCAAAAGGGAAGGGTAAAGTCGGACCAGTGTCAAGGAAAGTTTGT  
TTTATTGAGGTGGAAAAATAGCCCCAAGCAGAGAAAAGGAGGGTAGGTCTGCATTATAACTGTCTGTGTGAAGCAAT  
CATTTAGTTACTTTGATTAATTTTCTTTTCTCTTATCTGTGCAGTACAGGTTGCTTGTGTTACATGAAGATCATGC  
TATATTTTATATATGTAGCCCCAATGCAAAGCTCTTTACCTCTTGCTATTTTGTATATATATTTTCAGATGACATC  
TCCTGCTAATGCTCAGAGATCTTTTTTCACTGTAAGAGGTAACCTTTAACAATATGGGTATTACCTTTGTCTCTTC  
ATACCGGTTTTATGACAAAGGTCTATTGAATTTATTTGTXTGTAAGTTTCTACTCCCATCAAAGCAGCTTTCTAAGT  
TTATTGCCTTGGGTTATTATGGAATGATAGTTATAGCCCXTATAATGCCTTACCTAGGAAA

**FIGURE 14**

GTCATATTGAACATTCCAGATACCTATCATTACTCGATGCTGTTGATAACAGCAAGATGGCTTTGAACTCAGGGTCA  
CCACCAGCTATTGGACCTTACTATGAAAACCATGGATACCAACCGGAAAACCCCTATCCCGCACAGCCCACTGTGGT  
CCCCACTGTCTACGAGGTGCATCCGGCTCAGTACTACCCGTCCCCCGTGCCCCAGTACGCCCCGAGGGTCCTGACGC  
AGGCTTCCAACCCGTCGTCTGCACGCAGCCCCAAATCCCCATCCGGGACAGTGTGCACCTCAAAGACTAAGAAAGCA  
CTGTGCATCACCTTGACCTTGGGGACCTTCCTCGTGGGAGCTGCGCTGGCCGCTGGCCTACTCTGGAAGTTCATGGG  
CAGCAAGTGCTCCAACCTCTGGGATAGAGTGCGACTCCTCAGGTACCTGCATCAACCCCTCTAACTGGTGTGATGGCG  
TGTCACACTGCCCCGGCGGGGAGGACGAGAATCGGTGTGTTGCGCTCTACGGACCAAACCTTCATCCTTCAGATGTAC  
TCATCTCAGAGGAAGTCCTGGCACCTGTGTGCCAAGACGACTGGAACGAGAACTACGGGCGGGCGGCCTGCAGGGA  
CATGGGCTATAAGAATAATTTTTACTCTAGCCAAGGAATAGTGGATGACAGCGGATCCACCAGCTTTATGAACTGA  
ACACAAGTGCCGGCAATGTCGATATCTATAAAAACTGTACCACAGTGATGCCTGTTCTTCAAAGCAGTGGTTTCT  
TTACGCTGTTTAGCCTGCGGGTCAACTTGAACCTCAAGCCGCCAGAGCAGGATCGTGGGCGGTGAGAGCGCGCTCCC  
GGGGGCTGGCCCTGGCAGGTCAGCCTGCACGTCCAGAACGTCCACGTGTGCGGAGGCTCCATCATCACCCCGAGT  
GGATCGTGACAGCCGCCCACTGCGTGGAAAACTCTTAACAATCCATGGCATTGGACGGCATTGCGGGGATTTTG  
AGACAATCTTTTCATGTTCTATGGAGCCGGATACCAAGTACAAAAGTGATTTCTCATCCAAATTATGACTCCAAGAC  
CAAGAACAATGACATTGCGCTGATGAAGCTGCAGAAGCCTCTGACTTTCAACGACCTAGTGAAACCAGTGTGTCTGC  
CCAACCCAGGCATGATGCTGCAGCCAGAACAGCTCTGCTGGATTTCGGGTGGGGGGCCACCGAGGAGAAAGGGAAG  
ACCTCAGAAGTGCTGAACGCTGCCAAGGTGCTTCTCATTGAGACACAGAGATGCAACAGCAGATATGTCTATGACAA  
CCTGATCACACCAGCCATGATCTGTGCCGGCTTCCTGCAGGGGAACGTGATTCTTGCCAGGGTGACAGTGGAGGGC  
CTCTGGTCACTTCGAACAACAATATCTGGTGGCTGATAGGGGATACAAGCTGGGGTTCTGGCTGTGCCAAAGCTTAC  
AGACCAGGAGTGACGGGAATGTGATGGTATTCACGGAAGTGGATTTATCGACAAATGAAGGCAAACGGCTAATCCAC  
ATGGTCTTCGTCCTTGACGTCGTTTTACAAGAAAACAATGGGGCTGGTTTTGCTTCCCCGTGCATGATTTACTCTTA  
GAGATGATTCAGAGGTCACTTCATTTTTATTAAACAGTGAACCTGTCTGGCTTTGGCACTCTCTGCCATACTGTGCA  
GGCTGCAGTGGCTCCCCTGCCAGCCTGCTCTCCCTAACCCCTTGTCGCAAGGGGTGATGGCCGGCTGGTTGTGGG  
CACTGGCGGTCAATTGTGGAAGGAAGAGGGTTGGAGGCTGCCCCATTGAGATCTTCCTGCTGAGTCCTTTCCAGGG  
GCCAATTTTGGATGAGCATGGAGCTGTCACTTCTCAGCTGCTGGATGACTTGAGATGAAAAAGGAGAGACATGGAAA  
GGGAGACAGCCAGGTGGCACCTGCAGCGGCTGCCCTCTGGGGCCACTTGGTAGTGTCCCAGCCTACTTCACAAGGG  
GATTTTGCTGATGGGTTCTTAGAGCCTTAGCAGCCCTGGATGGTGGCCAGAAATAAAGGGACCAGCCCTTCATGGGT  
GGTGACGTGGTAGTCACTTGTAAGGGGAACAGAAACATTTTTGTTCTTATGGGGTGAGAATATAGACAGTGCCCTTG  
GTGCGAGGGAAGCAATTGAAAAGGAACCTGCCCTGAGCACTCCTGGTGCAGGTCTCCACCTGCACATTGGGTGGGGC  
TCCTGGGAGGGAGACTCAGCCTTCCTCCTCATCCTCCCTGACCCTGCTCCTAGCACCTGGAGAGTGAATGCCCCCTT  
GGTCCCTGGCAGGGCGCCAAGTTTGGCACCATGTCGGCCTCTCAGGCCTGATAGTCATTGGAAATTGAGGTCCATG  
GGGGAAATCAAGGATGCTCAGTTTAAGGTACACTGTTTCCATGTTATGTTTCTACACATTGATGGTGGTGACCCTGA  
GTTCAAAGCCATCTT

**FIGURE 15**

GGATTTCGGGGCTCCATGGCAAGATCCCTTCTCCTGCCCCCTGCAGATCCTACTGCTATCCTTAGCCTTGGAAACTGC  
AGGAGAAGAAGCCCAGGGTGACAAGATTATTGATGGCGCCCCATGTGCAAGAGGCTCCCACCCATGGCAGGTGGCCC  
TGCTCAGTGGCAATCAGCTCCACTGCGGAGGCGTCCTGGTCAATGAGCGCTGGGTGCTCACTGCCGCCCCACTGCAAG  
ATGAATGAGTACACCGTGCACCTGGGCAGTGATACGCTGGGCGACAGGAGAGCTCAGAGGATCAAGGCCTCGAAGTC  
ATTCCGCCACCCCGGCTACTCCACACAGACCCATGTTAATGACCTCATGCTCGTGAAGCTCAATAGCCAGGCCAGGC  
TGTCATCCATGGTGAAGAAAGTCAGGCTGCCCTCCCGCTGCGAACCCCTGGAACCACCTGTACTGTCTCCGGCTGG  
GGCACTACCACGAGCCCAGATGTGACCTTTCCTCTGACCTCATGTGCGTGGATGTCAAGCTCATCTCCCCCAGGA  
CTGCACGAAGGTTTACAAGGACTTACTGGAAAATTCCATGCTGTGCGCTGGCATCCCCGACTCCAAGAAAAACGCCT  
GCAATGGTGACTCAGGGGGACCGTTGGTGTGCAGAGGTACCCTGCAAGGTCTGGTGTCTGGGGAACTTTCCTTGC  
GGCCAACCCAATGACCCAGGAGTCTACACTCAAGTGTGCAAGTTCACCAAGTGGATAAATGACACCATGAAAAAGCA  
TCGCTAACGCCACACTGAGTTAATTAAGTGTGTGCTTCCAACAGAAAATGCACAGGAGTGAGGACGCCGATGACCTA  
TGAAGTCAAATTTGACTTTACCTTTCCTCAAAGATATATTTAAACCTCATGCCCTGTTGATAAACCAATCAAATTGG  
TAAAGACCTAAAACCAAAACAAATAAAGAAACACAAAACCCTCAA

**FIGURE 16**

CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAGAATTAATCGGAAAGCAGA  
AAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATAA  
GGACACGGGAGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTG  
ACTGCCCTTCAGAACTTCAGCACACACAGGAACCTCTTCCACAGTGGCACTTGCCAATTAATAATAGCTGCTATTATA  
GCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATTACCCTTTAGCAACTTCCCATCAACAATATTTTGA  
TAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAG  
GTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATG  
TTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGTCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAAT  
GAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTG  
AGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTG  
ACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTC  
CCTTCTACTGGGCACAATACACGCATTGATTTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATA  
CACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCTGCCATGC  
TTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAGATATGTTCCCA  
GTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTG  
TTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA



**FIGURE 17A**

GGTGGAGACACCGCCTCAGGGCTCGGTGCACAGTGGACATTTGGGGAGCGTTGTGGGTGACCCCCACACAGGCACTG  
 GGAATGCAGGGGAGAGGGGGCCAAGGGGAAAGGGGGCCAGAGTGTGGCTTTGGATTGAGGAGGGATGGATTCCAGT  
 CCTAGCTTGCCACTTATTAGGACTCCTGAGAGCAGCCTCCATGAGGCCCTGGACCAGTGCATGACCGCCCTGGACCT  
 CTTCTCACCACCAACAGTTCTCAGAAGCACTCAGTACCTCAAGCCCAGAACCAAGGAAAGCATGTACCACTCACTGA  
 CATATGCCACCATCCTGGAGATGCAGGCCATGATGACCTTTGACCTCAGGACATCCTGCTTGCCGGCAACATGATG  
 AAGGAGGCACAGATGCTGTGTGTCAGAGGCACCGGAGGAGTCTTCTGTAAACAGATTCCCTCAGCAGCCTGGTGAACCG  
 CCCCACGCTGGGCAATTCACTGAAGAGGAAATCCACGCTGAGGTCTGCTATGCAGAGTGCCTGCTGCAGCGAGCAG  
 CCCTGACCTTCTGTCAGGGTTCCTCACACGGAGGGGCGAGTCAGGCCCAGAGCCTTGCATGATCCCTCTCACGCCTGC  
 AGCTGCCACCTGGGCCAGGCCGTGACCATCTTTTCTCCTGTCAGGACGAGAACATGGTGAGCTTCATCAAAGCGCG  
 CATCAAAGTTCGAAACAGCTACCAGACCTACAAGGAGCTGGACAGCCTTGTTTCAGTCCCTCACAATACTGCAAGGGTG  
 AGAACCCCGCACTTTGAAGGAGGAGTGAAGCTTGGTGTAGGGGCCCTTCAACCTGACACTGTCCATGCTTCCTACT  
 AGGATCCTGAGGCTGTTGGAGTTTGTGGGGTTTTTCAGGAAACAAGGACTATGGGCTGCTGCAGCTGGAGGAGGGAGC  
 GTCAGGGCACAGCTTCCGCTCTGTGCTCTGTGTCATGCTCCTGCTGTGCTACCACACCTTCTCACCTTCGTGCTCG  
 GTACTGGGAACGTCAACATCGAGGAGGCCGAGAAGCTCTTGAAGCCCTACCTGAACCGGTACCCTAAGGGTGCCATC  
 TTCCTGTTCTTTGCAGGGAGGATTGAAGTCATTAAAGGCAACATTGATGCAGTGAGTGATGGGGGTCCGGGCCGGGG  
 CTGGGGATCCCTCGGGGTCTCCAGACCAGCAGGAAGTCAGGCACATGTGACATACTCAGGGACAGGATAGACTGGG  
 GGCGGGGGGGGGCCAAGAGAGAACCAACCAGAGAGCAGGGGCGAGGAGGCCCTTCTGGCAGAGCAGCCTGGGAAG  
 ACAAGGGAGGAGGAGGCATTTGTGGTGCCTGGGATTTTGAAGTGGGAGATATAGGACTGCAGCATTCAGTGAGGGA  
 GGTGGAGGGAGGTGCTTGAAGGGAGGCAGAGGTTAGGAAAGCCCATCTGTTTAGGGCATGACGATTAGGCTGGAGTCT  
 GGTACCTCCCTCCATTATAGCTCTCTCCTGCTCTTTCATTTTGTACTAAAAACAGAGTCTTAGGCGGGGGCTGT  
 ATTTGAGCCCAACGTGATGTAAGACTTAGGAGGTAAGAACAGGACTGGAGGCCAGATCTCCTGGCTCCTGGGGCCCC  
 ACCTGAGCCTAGCACAGGGCTGGACCACTATGCCCTGGAGGATCCCGGTCTGCTGTGGTGTGGGAGGTTTCGAGG  
 ATGCAGAGGGGTTGGGGCTGGGTGGGCACCCGTCAGGCTGACCAGAAGGTGCCTGCAGGCCATCCGGCGTTTCGAGG  
 AGTGCTGTGAGGCCAGCAGCACTGGAAGCAGTTCACCCACATGTGCTACTGGGAGCTGATGTGGTGCCTCACCTAC  
 AAGGGCCAGTGGAAGATGTCTACTTCTACGCCGACCTGCTCAGCAAGGAGAAGTCTGGTCCAAGGTGGGCTGATG  
 CCACGTGTTAGGGGCATTGGGTGACCAGGGCTGACTGTGTGCCTCCAGACCACGGGCCAAATCCCTAAGTGAACACA  
 GATGTCTCAGCTGGAATCTAACATAACCTTAAATCTAATAGGACTCAGGCTTGAAGGAAGTAAAGACCACAAGA  
 GAACTTCTGAACCAACAATGTGTACAAAGAGATTTCTAGTCACAAAGGACAGAAACATGGCTCCCTCTGTCCAGTA  
 GAACTGTTTCTGTGGTAGAAATGTCTACTTATGCACTGCCCAAATATGGTAGTCACAGCCACATGTGCACAAATGA  
 GCACATGAAATGTGCCTAGTGCAACTGGGAAACTGATTGTTTTAGTTTTATTTAATTTAATTAAGTAAATGTTAA  
 ATTTAAATAGCCATGTAGGGCTTGTGGCCACTATATTGGACTATGCAAGTCCAAAACACAAAAGGCTCATATAACTG  
 AACATTTCTGGCACATCCGACTTCAGGTAGGGCTGGATCCAGGAATTCAAATGATGTCGTCTGGCTTGGTCTTTCCA  
 TTTGTGGCTGTGCTCTCTCCTATGACATCTTGGTTTCTGCTGATCCTTTGCAGGAAGGTTCTTCCATGTGACAGGC  
 AAGGTGGCCACGGGCTGCTTCTACTCATATCCTCCCTTGGTTTTCAACCAGAGTCCACAGTTTGAGCCTCACTGGT  
 CTGACTTGTACCTGCCAATGCCTGGAACAGAGGGGTGGGAAGATTCTCATGGGCTGAGAGTAGGAGAGGGGTGGT  
 TCCACAGAAGAAAATGATGCACCCAGAAATAGTGGAGGGATTAAACAAGATGCCATACAGGCAAAACAAAGCCAAACA  
 GATGCCCCGCTACCAAAGATGAAATTTATCATGGTAAGTATTGAAATAAGTGTTAGCTTGTACCATCATAGTAATGA  
 TAGTGCAGAAATTGGAACCAAGAGTCTTACAACCACCTAGCTCAGCAAACGTCTAATCTGTTATTTGTAAATACACA  
 GGACATGTGTCTTCATGGCTTCATCCCTGCCCATAGCAGACATTGCTAATCAATCCTCTGCCATGAGCCTAGCTGT  
 GACCTTAGATACCTTCCCTGCAAAGCTCCAGGCAGCCGTTAGAAGTACCCACATTTGGCACCTGTTAGGAGACCTGT  
 CATCTGCATCTGGTCCCTCCCTCCTCTGCTGAGGCTCTTCCGTAGCCCTGCCTGGGGACCAAGCTGAAGGGG  
 AATTCTCTGGGTCTGGGGCAGGTGGGGCTGGGGAAGGGAGCAGGCTTCTACTGAGCTCTCAACATGTCTGGCACCTG  
 TCATGTCTCCACACCACACCCAGTGAGGAGAAGTTATTATCTCCATTGGGCACATGAGGGCCACTGATGCTAAGCG  
 AGGACTGTGACTTTCCACCCACATGGCTGTTGGTGACAGACCCGATTTGAGGACAGTCTGTGTGACTCAGAGG  
 CCTCTGCTTCTCTCTTGTCTCTAGAGTCCCTCCTGAGGAGTCGGGGCTTGCCCTGAGCCCACCCTGCTGTTGAAGGTG  
 CTTCTCAGGCCAGCTCCCATGGCCCCACACCCCTCCTCATCACCTCCTACTCCCAAAAGGACAAAAGCCTCAG  
 GGAACCTTTTTTCTTTTTTTAGAGACAGGGTCTTGCTATGTTGGTCAGGCTAGTCTTGAAGTCTGGGCCAAGCAA  
 TCTTCCACCTCTGCCTCCTAAAGTGTGGGATCTGGGCCTTAGGGAACCTTTTTGAAGTGAAGTGACTCTCGAA  
 GCCTTCTGTAGAGTGAGGTGGGTGGCTGGGGCTAACCATATGGGGAAGGAGAGACCTGGTGGGGGCACACAGCTGC  
 TATATAGAGGAACAGAAGGTGGGCCAGGCTCCAGCTGTGAGGAAATCTGGCTCAGTCCCCAGACCGCTGTGTGGC  
 TTTGGGGTGGCCAGTCCCTCTCTCTCTGCAACACTCTCCTCATGAGGACTTCTGTGAAAAATGGGGGTGTGAACCTT  
 CTGAGTCTGGGGCCCCACCAATTTCTAATCTCCAGAAGTTGGCCACCACAGACTCCACCAACTTCTAG

**FIGURE 17B**

TCCTGGGGCCTGGGCCTCTGGCCATTGCCATAGGCACCACTGCTCTGTGCAGGCAGCGCCCCCTCTGCCAGGATC  
CTCCGAGGTCAGCTGCTGGGTCTGACCCGCAGACCCTGGCTGAGCGACGGATGAACGGAGTATGCAGACACAGGCTT  
GCCTGTCTCAGCAGATGGGGGACCCCTGCCAGAGTCAGCAGCGGCCCCCATAAGCCTGCCACGCTTGCAATTTATTTAGT  
ACAGATGTAATGACAAAGGCCTAAAGCAAACCTCCATTTGTGGGTAATTAACATTGTGCCCCCCCCAGAAAGAGCAGT  
CCTCCGCATGATGATTAAAGGCCAGGTTCCGAGGCCTAAGTAAACCAACTTATCTAGATCAATTCCTTACTTCTTG  
TTATCTACTCTGAGAGAATTCAGCTGCCTTCAGCCAAATCCTTTCCCGAAGCTTTTGCAAAACCTCCGAGCCTTCCA  
AGGTTTGCTTCTTTCTGTAATTTTTCTCACCACCTGACCTATCTCCTGCAGTCAGCCCTGTGGAGGCCTTTGTGTT  
TCCCCCAGTGCTGGCAGCCTAGAGGCTGAGATGGCCAGAAACAAGGTGGTGACAGTGGCGTGCTCAGGGCTTGGGAA  
ACCCAAGGAGCTAAAGGCATGCCCAGGCAACCAAAGAGGACAGGAAGGCTTCTGAGGAGAGACCTCTGAGGTGGGTC  
TTGGAGAGGAAGGACTTAGGGAGGCAGAGTGGAGGAAGTGAGAGGACACCCCAAGCCAAGAGGGCGGCAGGACCAA  
GGCTCAGAAGCCAGGGCGCTGCAGAGGGGCTGTGTGCCACAGGGTGAAGAGTTTGTGTGGCAGAAGGGCAGGGGGCT  
TGCATCAGGGGTGACAGCTGCTCTTTTGTCCCAGCATAGCCCCTGTACATCCCTGGAGAGCTGGGGCGTCCACAAC  
CTAAGTCACAGCCCCATCCTAACCCCTGGTGGTGCAGTGAGGGTGAGCTGTCTGTGGGCAGGAGGGAAGACTCTTGG  
AGATGAGCCTGGTGAAGGGATAATGGCATCCCGGGCCGAGGAGCAGCACAGGCAGAGGCCTGGGGAGAGTTTAAGGA  
GTGTAGGGGAGGAAATGGCAGAAGATGAGCCAGAAAAAGAAAGGTTAGGGCAGGTCCTGGAGGACATGAGTGGCTGT  
TTGGGCTTTATCCAGCAGTGGGGGAGCCTTGGCAGGCTTGTGGCTTAGATAGGTGCTTTAGAAAGCCACACAGCAGT  
TGCTGGGCCACCCGCTGGCTGGGTCTTCTAAGGCAGGAAATACAAGCATGAGCAGGAAAAGACCCCTCAAGG  
CTCACGTCCTAGTGGGGAGACAAGAAACACAGATGGGCAATATAACACGATGTCTGGTTCCAGTAAGTGCAGTGAAG  
AACAAGCGAGGCTGGATGCAGGGAGTGATGGGAGGGGCTTTGTAAGGGGAGGTCGGGGGAAGCCTGTCTCAGAGGAC  
ACCAGAATGGAGCGCAGGAGCAGCAGTGGCAGTCACATGGCAGGCCGTTAGGGCAGAGGGAGCTGGGCAGGGCACA  
GCAGGGCAGGAGTGTGTTTGATGTGTCTTGGGAACCGCCCTGAGGCCGTCGTGTGGCTGGAGTGTCTGCAGGTGTCAA  
GGAAATTGTAGGAGATGTCTCCTGAGTGTGATGGAATATAACCAGATTTCCAGAAGGAAGTACATGATCTGACTTA  
AAAAGGTCAGTGTGCGAAATGGCTTGCAGGGGACAGGAGTGGGAGCAGGGAGATAGGAGACAATGTGTACCAGGACA  
GCAGAAAGACATCCCGGGTAGCCTGGAACAGGGAGACGGTGTGGAGATGGTGGCAGTCCGATAATGAGAGCCGTAGG  
GCAAGGCCAGCAGGATCCTAGAGTGAGACGGGAGGTAAAGTCACCGGGACTTGGTGTCTCCACGTGAGGGGCAGGGG  
AAAGGGAGAGGACAAGGGTGACCCGGGAGGTTAAAGATGGGACCGGGGCCAGACGCAGTGGCTCATGCCTGTAATCC  
TAGCACTTTGGGAGGCTGAGGCGGGCGGATAGCTTGAGGTGAGGAGTTTGAAACCAGCCTGGCCAACATGGTGAAAC  
CCCGTCTCTACTAAAATATACAAAAATTAGCCTGGCGTGGTGGTGCATGCCTGCAGTCCCAGCTATTCAGGAGGCTG  
AGGCAACAAGAATCGCTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCGCCATAGCACTCCAGCCTTAG  
CCTGGGCGACAGAGCGAGACCACATC

**FIGURE 18**

GAGCAGCGGGCCTGACGGGACCAAGGCGGGAGTCTGCGGTCGTTCCCTCGGCTGTGGACCGGGCGGCACGCAC  
 GCGGTGCAGGGTAACATGGCGGATGCGGAAGTAATTATTTTGCCAAAGAAACATAAGAAGAAAAAGGAGCGGAAGTC  
 ATTGCCAGAAGAAGATGTAGCCGAAATACAACACGCTGAAGAATTTCTTATCAAACCTGAATCCAAAGTTGCTAAGT  
 TGGACACGTCTCAGTGGCCCCTTTTGCTAAAGAATTTTGATAAGCTGAATGTAAGGACAACACACTATACACCTCTT  
 GCATGTGGTTCAAATCCTCTGAAGAGAGAGATTGGGGACTATATCAGGACAGGTTTCATTAATCTTGACAAGCCCTC  
 TAACCCCTCTTCCCATGAGGTGGTAGCCTGGATTTCGACGGATACTTCGGGTGGAGAAGACAGGGCACAGTGGTACTC  
 TGGATCCCAAGGTGACTGGTTGTTTAATCGTGTGCATAGAACGAGCCACTCGCTTGGTGAAGTCACAACAGAGTGCA  
 GGCAAAGAGTATGTGGGGATTGTCCGGCTGCACAATGCTATTGAAGGGGGACCCAGCTTTCTAGGGCCCTAGAAAC  
 TCTGACAGGTGCCTTATTCCAGCGACCCCCACTTATTGCTGCAGTAAAGAGGCAGCTCCGAGTGAGGACCATCTACG  
 AGAGCAAAATGATTGAATACGATCCTGAAAGAAGATTAGGAATCTTTTGGGTGAGTTGTGAGGCTGGCACCTACATT  
 CGGACATTATGTGTGCACCTTGGTTTGTATTGGGAGTTGGTGGTCAGATGCAGGAGCTTCGGAGGGTTCGTTCTGG  
 AGTCATGAGTGAAAAGGACCACATGGTGACAATGCATGATGTGCTTGATGCTCAGTGGCTGTATGATAACCACAAGG  
 ATGAGAGTTACCTGCGGCGAGTTGTTTACCCTTTGGAAAAGCTGTTGACATCTCATAACCGCTGGTTATGAAAGAC  
 AGTGCAGTAAATGCCATCTGCTATGGGGCCAAGATTATGCTTCCAGGTGTTCTTCGATATGAGGACGGCATTGAGGT  
 CAATCAGGAGATTGTGGTTATCACCACCAAAGGAGAAGCAATCTGCATGGCTATTGCATTAATGACCACAGCGGTCA  
 TCTCTACCTGCGACCATGGTATAGTAGCCAAGATCAAGAGAGTGATCATGGAGAGAGACACTTACCCTCGGAAGTGG  
 GGTTTAGGTCCAAAGGCAAGTCAGAAGAAGCTGATGATCAAGCAGGGCCTTCTGGACAAGCATGGGAAGCCCACAGA  
 CAGCACACCTGCCACCTGGAAGCAGGAGTATGTTGACTACAGTGAGTCTGCCAAAAAAGAGGTGGTTGCTGAAGTGG  
 TAAAAGCCCCGAGGTAGTTGCCGAAGCAGCAAAAAGCTGCGAAGCGGAAGCGAGAGAGTGAGAGTGAAAGTGACGAG  
 ACTCCTCCAGCAGCTCCTCAGTTGATCAAGAAGGAAAAGAAGAAGAGTAAGAAGGACAAGAAGGCCAAAGCTGGTCT  
 GGAGAGCGGGGCCGAGCCTGGAGATGGGGACAGTGATACCACCAAGAAGAAGAAGAAGAAGAAGCAAAAGAGG  
 TAGAATTGGTTTCTGAGTAGTGAAGGCCACTTGAAGCTGGAGGAGAACTAAAGCCTTATTGAGAAAACATGTTATA  
 GATCCTTTTGTGCTGAGAGAGTGGAACATAGGTCTAGACAGGGTGAAGAGTTCTGGCACATTTTAGCTGCTACTT  
 TGAGACCTCGGTGATGTTACCTGGTGTGGTCATCCCATCTTGTCTGTTTTAAGGATATGGGTGGTGAAAGATGAAA  
 GAGGCAGAGTTTATCCCAATGACTTCTCTGTTTGAGTTGGGAAGCCTCACCTTCAGACCCAGTAACCTGTCCGCAGCT  
 GTCTGCTAGTGTTGTCTTAACATCGTAGTCCTAGTTTGCATTTTTTAAATCCCTCTGTTTAAAAGGTTTGTAAAA  
 CAAAAACAAAAAACTAAGTCTGCTCAGTGAAATGCTGTAGAACCCTAAATAAGTGGTAGAAGAGTGTCACCTGAATTT  
 TGTCTCTGAATTCAGTATAACTGAGTTTGTCCATGCTGGTGTCTGGGTTATAGGCCTGATGGGCCTGGTAGTTTTC  
 CATCTTGTCTGGCCTAGAGGTCAGTCCTTTGCACTTCCTCAAAGCTTGTGTACAGTGCTCACCTAAATCCATCTGA  
 CTACTTGTTCCTGTGCCCTCTTGTTTTAGGCCTCGTTTACTTTTTAAAAAATGAAATTGTTTCATTGCTGGGAGAAGAA  
 TGTGTGAATTTTTACTTATTAAAGTCAACTTGTTAAGTTTTTTATGTATTCTGTTGGGTTTTCTTGTGATCTCAT  
 GCTAGCAGAGCAAAAATTGTAAATATTTTGATTAAAAATCTAGGGACCTTTATGTCTATTGGAATTGATATCAA

**FIGURE 19**

GGCACGAGGCTACAAAGCAGGAAAGTATGCTTGGGAGAGGCCAAGTGAGTGGGGAATCAGCCCAAAGCCAGGCGTCC  
AGGGTCTCCCTCACCTGAAGCTGACTTTTTCCCCACCTTGGACAGAGGGCGGGAGATGCCATCCCCACTGAACCCAG  
TGCTTTCACCAGCCATATTAGCTCCCACTCACCCCCCGTCGTGGAAGCCTCGGCCGTACACCTGCAGGGCCGGGGC  
GTGCATGGCCTCAGGGATGGCCTGTTGAGCTGCTGGGTGACTCGGGTCCAGGTGCCTCACCACCTGCTGAGCTCTGT  
GTGATTTCTGGACGCTTCTGCTCGTTGCCTTTGGGCTCAGTGAAGAGTCTGGAGTTTATCTGGAGTGAGGTGGCCGG  
TTCTTGGTGGGATCTGAGCAGGACAGCGTCTGGCTCCTTCCCTCGGCTCATGGCCCTCAGAATCTGCGTCACATACA  
CCCCAGCTCTCCCGATAGGTCTCTGCACTCGCTGTTGCCTCTGCCTGGAACAGTCTCCCTCCTGGTGTCATTGTCTC  
CGTGGTGCTCCTTCCCTGACCTTCCACCTCCACAGTCTGTCCCCCTTGGGGACAGGGACTCGTTGCTCATGTTTAC  
CCGGCAGGCTGGACACTTCGTGGAGGGCTCCAAAGCTGGCAGATCCCGGGCCGCTCTGTCTCTCCAGGCCCTGC  
GTGTTGCGGTGAGAGGAGCATTGTGTCTCTGTGGTTTGTGCTGGAGCTGGTGACCGGGAGAGAAACAAGGGAGAC  
AAGGGTGCCAGACAGGTGCGGGCTCAGCCAGGAGGCAGAAGACGTGGACGTGTCCCGGGCCAGGAGGGTCACAGA  
TGACCAACAAGGCACTCTGTGTGGCACTGGGAACAGGAATTCTGGGAGTCAGTCTGCAAGGGCGGTGGGCGTTGCTC  
ACCTGGGAGAAGCCTTTAGAGTGGGCGTTGAGCAGGCCATTAGCTCGTGCCCTGAGGAGGTGCATGGGCGGCATGGG  
CTCTCCATGAAATTATGTGGGCGCGAATGGATGTGGCTCTGCGCTCACCTGGGCGAGGACTTCTGGCCGGTGCCGG  
GGCACTCTCGGTGACCCTGGCAGAATCGAGCTGCCCTGACTATGAAAGGGGAAGAAGAGCATGCCTGACCCTCCACC  
GGCACCCACCCCTCACTGCTCCACCTGGGGCCTGCCTCTGCGGGTGGCTGGGTCTGGCTGACTGTTGTGACTGTT  
GAGGCCCTGGGGGGTGGGCGCATGGGAGTTAGGAGGACTGGCCAGGTGGGGCCACTATGCACCCACCCCAAGTGTC  
AGGTGCTTCTCCTCTCCTCCTCCACCACCTCCTCCTCCTCCTCATCATCATCCTCACTTGTTGAGGACGTCCTG  
TGTGCCAAGTGGTTTATATGCCCAGCCTCATTTAATCCTCAGAATGACTCCATGAGGTAGCTACTAAACCCCCAC  
TTAACAGATGAGGAACTGAGGCCTAGAGAAGCTCAATAAGTTGCCTAAGTTCCAAGTTTCTCTCCCAACTCTCCT  
ACCTCTCCTCTTCTCCTTTCTCCCATTTCTTCCCTGCCTCTTCCCTAACTAGACAATTTTTTATTGAGTGTCT  
CCCAGGTGCAGGCATGAGCCAGGTGCTGGGAAAATCATGATAACCCAGCTCCTTCTGGTCATTTTCTCAGCTGGTTA  
GAGGCTGGGAGGACACGCAAGTTCAGCTCCAGCCGACTGGGGCATTGGTGGTAGCCCCTGGAGACATTGTGCAATGG  
GGCTACGAGGCTGCATCTGGCTCCAGGGAAGCGTGTGCAATCCATGAGTGATGTCTGCCATGCGTACAGGCATGGA  
GAGTGAGGCGCCTGTACTGTCTTTCTGTAGACCCTAGACTGGTGGGGCCTCTGAAATGCATCCAGACACTGTGCTGG  
GTGTGTTGCATGGCCCTCCCAACCAATTGAGTATTTTCTCCCCATTTTCCAGGGAGAAATCTAAGGCGTCAGAATG  
TAAGGTTCTTATTGGAACCCAGGCTCCAGGGTCCCTGGTTTTCTGTGACATCATGCTGCAGGACCCTGTTTCTCTCT  
TTGCTTTGGCTGCTGGGGAGCTCAGAAGGGAGCTTTAGGCTTGCTCTCAGTCACCACATTAGCTCAGGGGTTTGGGC  
ATTTTGTGCGCGTCTCCTTTGGGCTCTGTCTCCTCCCTGCTGTGCTTCTGAGGAGCAGGCCGGATGTAAGTTATC  
AACTATAAAATAAAACCAAGACTTCCGTTCTGGCTCTCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 20**

GTACAGAAGCAAAATCAAACCTGCTATTTTCAGCACTCCTGTTTTTAACTTGGTGTCTTTAGTGCTTGGATTGGTGGG  
 ATGTTTCGGAAATGGGCATTGTGCGCAATTTTCAGGAGTTAGCTGTGCCAGTGGTTCATGACGGGGGCGCTCTTTTGG  
 CCTTTGTCTGTGGTGTGCTGTACACGCTCCTACAGTCCATCATCTCTTACAAATCATGTCCCCAGTGGAACAGTCTC  
 TCGACATGCCACATACGGATGGTCATCTCTGCCGTTTCTTGCGCAGCTGTATCCCCATGATTGTCTGTGCTTCACT  
 AATTTCCATAACCAAGCTGGAGTGGAATCCAAGAGAAAAGGATTATGTATATCACGTAGTGAGTGCGATCTGTGAAT  
 GGACAGTGGCCTTTGGTTTTATTTTCTACTTCCTAACTTTTCATCCAAGATTTCCAGAGTGTCAACCCTAAGGATATCC  
 ACAGAAATCAATGGTGATATTTTGAAGAAAGAAGAATTCAGTCTCACTCAGTGAATGTCGAGGCCATTTCTAAAAGT  
 GCTACAGAGGACAGACAGGGTTTTGAGGCCACCCTGATTATTGGGATGCATCTGCAGCACATCCAGGACTTGAATTT  
 CATTACGAGTTCCTAATAGTTGTATTTCTAAAGATGTGTTTCTTAGAGAATGTACAGCCTTATGACACTGTAGTGAT  
 GTTTTTATAATTTTCTAAGTAGATTTTTTATATTAACAAATTCATATACAGAAAAATAAGGTGTTACAAAAAATG  
 GAGAGCTCTTATTTTGTACAGATTCTGTCGTTTTTTTTTATTTGTGTGAGATTTATGGAAATACACTAAATGAGTA  
 ATTCAGGTTTCAGTACATTTATTACAAAGTGAAATCAGGGGATATTCATTTGTAAATTTTATTCTTAGTGAATGAAC  
 GTATAATTTTTTTTATCAGGAGAGCACTTATAAAATTCATTTATAAAGATCATATACCCAAATCATAAAGATTTAG  
 TTGATACATTAACACTAAGATACTCTGATTTTAGCGAACTAAACAAAGTGCTTCTACTGAGAGGCCTTTATACCAC  
 CATGTACAGTAACTCTAAGTGAATACGGAAGACCTTGGTTTTGAAATTCGCCACCTTGTTTCTCCCTGCTCATGAG  
 GTCGCACCTTTTGCTCTTGCTGCTAATTGCCATTTCGTAGTGGGTGTAATGCCAGGTGGAATGGTTTCAACAAGTCA  
 GGTGAAAACCATCCTTTATTGTTGCTGGCACAACCTTGATATATAGTCTGACTCAGAACTGAAGCTCACATCTCAAAT  
 TCATTTTCATGCCAGTAAATGTGGCAAAGAGAAGAAAGGCCCAAGAGCGAGACAAGAAGAATGGAGAAGGGGGCAGCC  
 AAGAAGAACCTTGGGTTTCAGGGTACTGTTTATTTGCTCCTTCTCTTCATGCCTGTGGCTGGATGTCCACAACACT  
 ATAAGAAATATAAGTCAAGCCCTTTGTGTTAAGCAAGAACTACAGACTCCATCTTTTACCCAAATCATGAATGACC  
 AATAAAAAGCAAGTTATTCCAGAGGAAGAAGCAGCCCTTGAAATGTTAAGGCTTAGGCTTGAAAGGTGAAGAGCAGG  
 AATTCTCTCTTTCAAATCCTAGAGCATAAACCCATGTGTGGCCAAGTGAGATCAGCCCTCAAGGGCACATGCCAAGG  
 GCAGAGCAGCCCATGTAGACAGCTTCGGAGGGCATGGGGGTGTAGGGAGTTCGGGGTAGCTCCTCATTAACATTTTG  
 TTGGGTGAGTAAAGGGGTGAGGCTCAGTGGCAGGTACCTCTGCAATGACAAGCTGCCTCCCCTCTATGTGTTTAGCA  
 TATGTTATTAGAACATGTCCGACACCCCTACCGCTGCCATTTGGGCCCTTTAATAAAGCCAAGTAGAGAAATCTGGC  
 AATAAAAGGCAAAATGTAAGCATGCTTTCTTTAAGACGCATCATAAATGGTTTTCTTTAAGTGAATGGAAGAGTTTGA  
 CAGAGATACACCTTTGTAAGAAAACATTAAGAATGCTGGCTGGCTGTGGTGGCTCACACCTGTATTTCCAGCACTTT  
 GGGAGGCCTAGGCAGGAGGATTGCTTGAGCCTGGGACTTCGAGACCAGACTGGGAAACATGGCAAAATCCCATCTCT  
 ACAACAAAAATACAAAAATTAGCCAAGTGCGGTGGTGTGCCTGTAGTCCTAGTTACTTGGGAGGCTGAGGTGGGAGA  
 ATCACCTGAGCCCAGGAGGTGGAGGCTGCAGTGAGCCATGCCAATGCACTCCAGTCTGGGCAACAGAGTGAGACCTT  
 GTCTCAAAAATAAATAAATAAATAAATGAATAAAGAGAATGCTAATCATTTCTGGGTTCACTGCGACTCACTGTAGT  
 GCTGGGGATCCCCCTTGTAACACTGGAAGTGAAGGCAGTGATGAAAGCTATGTCAAGCATTCAATTATTTCTGAAGAG  
 GAGGAGAAATGCCACATACCTTTCCCATGGGACCTGTGGTGGAATGAATCCATACTTCTGCCTCACTTCGAGCAGAC  
 TTTTGTCTCGGCGCTCCTCACGATGGAGTTTCATGCTTCATTTTACATCTCTCTGCACAATTAGATTGGGAGCTC  
 CTTGAGGGCAGAGTACGTGCCTTAATCTTTATCTTTGTAATGCCACAATGAACAGAGTGCCTCCTGGTACACTGTAG  
 GAGCTTAAGAAATACTCACTGAATGCATGAATGAATGAATGAACAAATGAAGGAATGACTAAGGATGTTTGTAGTGC  
 TATAATATAGAATGGGATTTACTCTGCTTTACCAGTTAGTTTCATAATAACAAATAGTCTGT

**FIGURE 21**

GGCACCGATTGCGGGCCTGCCCGGACTTCGCCGCACGCTGCAGAACCTCGCCCAGCGCCACC**ATG**CCCCGGCAGCT  
 CAGCGCGGCGCCGCGCTCTTCGCGTCCCTGGCCGTAATTTTGCACGATGGCAGTCAAATGAGAGCAAAAGCATTTTC  
 CAGAAACCAGAGATTATTCTCAACCTACTGCAGCAGCAACAGTACAGGACATAAAAAACCTGTCCAGCAACCAGCT  
 AAGCAAGCACCTCACCAAACCTTTAGCAGCAAGATTCATGGATGGTCATATCACCTTTCAAACAGCGGCCACAGTAAA  
 AATTCCAACAACCTACCCCAGCAACTACAAAAACACTGCAACCACCAGCCCAATTACCTACACCCTGGTCACAACCC  
 AGGCCACACCCAACAACCTCACACACAGCTCCTCCAGTTACTGAAGTTACAGTCGGCCCTAGCTTAGCCCCCTATTCA  
 CTGCCACCCACCATCACCCCACCAGCTCATACAGCTGGAACCAAGTTTCATCAACCGTCAGCCACACAACCTGGGAACAC  
 CACTCAACCAGTAACCAGACCCACCTTCCAGCAACTTTATCGATAGCACTGCACAAAAGCACAACCGGTCAGAAGC  
 CTGATCAACCCACCCATGCCCCAGGAACAACGGCAGCTGCCCAACAATACCACCCGCACAGCTGCACCTGCCCTCCACG  
 GTTCCTGGGCCACCCCTTGACCTCAGCCATCGTCAGTCAAGACTGGAATTTATCAGGTTCTAAACGGAAGCAGACT  
 CTGTATAAAAGCAGAGATGGGGATACAGCTGATGTTCAGAGCAAGGAGTCGGTTTTTTTACCTCGGAGATACTTCA  
 ACATCGACCCCAACGCAACGCAAGCCTCTGGGAACCTGTGGCACCCGAAAATCCAACCTTCTGTTGAATTTTCAGGGC  
 GGATTTGTGAATCTCACATTTACCAAGGATGAAGAATCATATTATATCAGTGAAGTGGGAGCCTATTTGACCGTCTC  
 AGATCCAGAGACAGTTTACCAAGGAATCAAACATGCGGTGGTGATGTTCCAGACAGCAGTCGGGCATTCTCTCAAGT  
 GCGTGAGTGAACAGAGCCTCCAGTTGTCAGCCACCTGCAGGTGAAAACAACCGATGTCCAACCTTCAAGCCTTTGAT  
 TTTGAAGATGACCACCTTTGGAAATGTGGATGAGTGCTCGTCTGACTACACAATTGTGCTTCCGTGATTGGGGCCAT  
 CGTGGTGTGCTCTGCCTTATGGGTATGGGTGTCTATAAAATCCGCCTAAGGTGTCAATCATCTGGATACCAAGAA  
 TCT**TAAT**TGTTGCCCGGGGGGAATGAAAATAATGGAATTTAGAGAACTCTTTCATCCCTTCCAGGATGGATGTTGGGA  
 AATTCCTCAGAGTGTGGGTCCTTCAAACAATGTAAACCACCATCTTCTATTCAAATGAAGTGAGTCATGTGTGATT  
 TAAGTTCAGGCAGCACATCAATTTCTAAATACTTTTTGTTTATTTTATGAAAGATATAGTGAGCTGTTTATTTTCTA  
 GTTTCCTTTAGAAATATTTTAGCCACTCAAAGTCAACATTTGAGATATGTTGAATTAACATAATATATGTAAGTAGA  
 ATAAGCCTTCAAATTATAAACCAGGGTCAATTGTAACATAACTACTGTGTGTGCATTGAAGATTTTATTTTACCC  
 TTGATCTTAACAAAGCCTTTGCTTTGTTATCAAATGGACTTTCAGTGCTTTTACTATCTGTGTTTTATGGTTTCATG  
 TAACATACATATCTCTGGTGTAGCACTTAACCTCTTTCCACTTTAAATTTGTTTTTGTGTTTTTGAGACGGAGTTTC  
 ACTCTTGTCACCCAGGCTGGAGTACAGTGGCAGCATCTCGGCTTATGGCAACCTCCGCCTCCCGGGTTCAAGTGATT  
 CTCCTGCTTCAGCTTCCCGAGTAGCTGGGATTACAGGCACACACTACCACGCCTGGCTAATTTTTGTATTTTATTA  
 TAGACGGGTTTCACCATGTTGGCCAGACTGGTCTTGAACCTTGACCTCAGGTGATCCACCCACCTCAGCCTCCCAA  
 AGTGCTGGGATTACAGGCATGAGCCATTGCGCCCGGCTTAAATGTTTTTTTAAATCATCAAAAAGAACAACATATC  
 TCAGGTTGTCTAAGTGTTTTTATGTAACCAACAACAAAAGAACAATCAGCTTATATTTTTTATCTTGATGACTCCT  
 GCTCCAGAAATGCTAGACTAAGAATTAGGTGGCTACAGATGGTAGAACTAAACAATAAGCAAGAGACAATAATAATG  
 GCCCTTAATTATTAACAAAGTGCCAGAGTCTAGGCTAAGCACTTTATCTATATCTCATTTTCTCACAACCTTATA  
 AGTGAATGAGTAACTGAGACTTAAGGGAACCTGAATCACTTAAATGTCACCTGGCTAACTGATGGCAGAGCCAGAGC  
 TTGAATTCATGTTGGTCTGACATCAAGGTCTTTGGTCTTCTCCCTACACCAAGTTACCTACAAGAACAATGACACCA  
 CACTCTGCCTGAAGGCTCACACCTCATACCAGCATACGCTCACCTTACAGGGAAATGGGTTTATCCAGGATCATGAG  
 ACATTAGGGTAGATGAAAGGAGAGCTTTGCAGATAACAAAATAGCCTATCCTTAATAAATCCTCCACTCTCTGGAAG  
 GAGACTGAGGGGCTTTGTAAACATTAGTCAGTTGCTCATTTTTTATGGGATTGCTTAGCTGGGCTGTAAAGATGAAG  
 GCATCAAATAAACTCAAAGTATTTTTAAATTTTTTGTATAATAGAGAACTTCGCTAACCAACTGTTCTTTCTTGAG  
 TGTATAGCCCCATCTTGTTGTAACCTTGCTGCTTCTGCACCTTCATATCCATATTTCTATTGTTCACTTTATTCTGTA  
 GAGCAGCCTGCCAAGAATTTTATTTCTGCTGTTTTTTTTGCTGCTAAAGAAAGGAACCTAAGTCAGGATGTTAACAGA  
 AAAGTCCACATAACCCTAGAATTTCTTAGTCAAGGAATAATTCAAGTCAGCCTAGAGACCATGTTGACTTTCTCATG  
 TGTTTCCTTATGACTCAGTAAGTTGGCAAGGTCTGACTTTAGTCTTAATAAAACATTGAATTGTAGTAAAGGTTTT  
 TGCAATAAAAACTTACTTTGG

**FIGURE 22**

CAGAGGTAGCCTGAAAGAAGCAGGAACTCCAGGATCCCAAACCAGAGCAGACCCTATAGTAAAGTATTTTTACATCT  
TTTCCTTTCCCCAGAAGAGATCCCTAACCTATTGTTTTATTGACAGCCTTGCTGTTAGAGGCTCTTTCCAGAAGTT  
GGACGAAGAGGCTCAGGCGTTGCTGTTTCTTGCTTCCAAGTCAAGTGGTTACTCTGGTAATGGATTGCCTCTCTCC  
GAGCTTTCACCCTGGTGAGACTGTCCAGATCTAGTCTGTAAACCCAGCTTAGAAGCACTGTTGTAAAAATGACTGAA  
GAGCCCATCAAGGAGATCCTGGGAGCCCCAAAGGCTCACATGGCAGCGACGATGGAGAAGAGCCCCAAGAGTGAAGT  
TGTGATCACCACAGTCCCTCTGGTCAGTGAGATTGAGTTGATGGCTGCTACAGGGGGTACCGAGCTCTCCTGCTACC  
GCTGCATCATCCCCTTTGCTGTGGTTGTCTTCATCGCCGGCATCGTGGTCACCGCGGTGGCTTACAGCTTCAATTCC  
CATGGGTCTATTATCTCCATCTTTGGCCTGGTTGTTCTGTCTGCTGACTTTTTTTTACTAGCCTCCAGTGCCTTGCTG  
CTGGAAGTGAGACAAAGGAGCAAGAAAGCCAAGAGACGGGAGAGTCAAACAGCTCTCGTGGCAAATCAGAGAAGCT  
TGTTTGCTTGAAGACTGAATACGACCAAATGGGCCATTGGGCCTGGAAAACGTGCTCTGACTTTGTACCCCAATTCAC  
CCAGAACCATGGTGGGAGAGAACAGACTTGGCGTTGGAGCAGACTGGAAGAATGGGGGTGGGAGGGTGGAGGGGGCTT  
CTCCTTTGTGAGGAATGACTCATGTCTTCTTTAACGACAACTTAACCCTAAGGGCTACTTCTGAGACTGAAAAATC  
AGCTTTCATTTACATGAAACACTTTGGGGGTCATGGGAGTGCACAGCATTAGACAGTATTTGGTTCACCCTGTAAA  
GTAGCCAAGAAAAGATGAGAAAAATCAAGATAGGCCTGGCACACTAGACATTTGCCTCCAAAAGAAATAACCTACAG  
TCTTAAGATGTATCATAAAAATGTTCTGCCAAGGATCTAAATTACCTTGGGTTTCGCATATGCTATGAAATTCTGT  
GATAATTTTTTTCAATACATTGATTCAGTGGCGTCTGTTTTTCATTTTATACTTTTAATAACTCATCACTGGTGGTAC  
TTTATCTTGAAAAGTAATATTTTTTATATTTTAACATTGGACAGTGTAGCCAGTTGTAATGATGTATCAGAAGTAA  
AGAAAAACCCATTAAAGTTATAGCTAATAGATGCTGTTGGGGGTAAATTAATAGTAAAATAATCCAATATAGCACT  
TTTGATGATTTTTATATAAAAGTCAACTGTACATTTCAATTCAGAATAATAAATACTTATTGCTGCTAAAACCTCTTA  
AATGGTTGTTTCTGCTATAGTTATTTCTATTGCAGTTCCAAATTGCCATCTTCCCTTGCTCTCATTTGCAAGTTCTCA  
ATTGTATTTCTCTCAAATGGACAGGTTCTTCTTTACTGGAGGATTTTTGTTTTTATCATATTGGTTTTTTCATTACT  
TCTGAATAGTCTTAATTACGTTTACTAAATTCTAAAGGATTTCTGTGCTATTATAATTAGGAAATCAACGTCTTTGG  
TCAGGAACTTTATAATGTGCTATTAAATGTATATTACATTTTTTGTGG

**FIGURE 23**

ATGCTGTCACTGCTCCACGCATCAACGCTGGCAGTCCTTGGGGCTCTGTGTGTATATGGTGCAGGTACCTAGAGCA  
ACCTCAAATTTCCAGTACTAAAACGCTGTCAAAAACAGCCCGCCTGGAATGTGTGGTGTCTGGAATAACAATTTCTG  
CAACATCTGTATATTGGTATCGAGAGAGACCTGGTGAAGTCATACAGTTCCTGGTGTCCATTTTCATATGACGGCACT  
GTCAGAAAGGAATCCGGCATTCCGTCAGGCAAATTTGAGGTGGATAGGATACCTGAAACGTCTACATCCACTCTCAC  
CATTCACAATGTAGAGAAACAGGACATAGCTACCTACTACTGTGCCTTGTGGGAGGTGCGGCTAGCCAACCAAGAGT  
TGGGCAAAAAATCAAGGTATTTGGTCCCGGAACAAAGCTTATCATTACAGATAAACAACTTGATGCAGATGTTTCC  
CCCAAGCCCACTATTTTTCTTCTTCAATTGCTGAAACAAAGCTCCAGAAGGCTGGAACATACCTTTGTCTTCTTGA  
GAAATTTTTCCCTGATGTTATTAAGATACATTGGCAAGAAAAGAAGAGCAACACGATTCTGGGATCCCAGGAGGGGA  
ACACCATGAAGACTAACGACACATACATGAAATTTAGCTGGTTAACGGTGCCAGAAAAGTCACTGGACAAAGAACAC  
AGATGTATCGTCAGACATGAGAATAATAAAAAACGGAGTTGATCAAGAAATTATCTTTCTCCAATAAAGACAGATGT  
CATCACAATGGATCCCAAAGACAATTGTTCAAAGATGCAAATGATACACTACTGCTGCAGCTCACAAACACCTCTG  
CATATTACACGTACCTCCTCTGCTCCTCAAGAGTGTGGTCTATTTTGCCATCATCACCTGCTGTCTGCTTAGAAGA  
ACGGCTTTCTGCTGCAATGGAGAGAAATCATAACAGACGGTGGCACAAGGAGGCCATCTTTCTCATCGGTATTG  
TCCCTAGAAGCGTCTTCTGAGGATCTAGTTGGGCTTTCTTTCTGGGTTTGGGCCATTTAGTTCTCATGTGTGTACT  
ATTCTATCATTATTGTATAACGGTTTTCAAACCAAGTGGGCACACAGAGAACCTCACTCTGTAATAACAATGAGGAAT  
AGCCACGGCGATCTCCAGCACCAATCTCTCCATGTTTTCCACAGCTCCTCCAGCCAACCCAAATAGCGCCTGCTATA  
GTGTAGACATCCTGCGGCTTCTAGCCTTGTCCTCTCTTAGTGTTCTTTAATCAGATAACTGCCTGGAAGCCTTTCA  
TTTTACACGCCCTGAAGCAGTCTTCTTTGCTAGTTGAATTATGTGGTGTGTTTTTCCGTAATAAGCAAAATAAATTT  
AAAAAATG



**FIGURE 24**

GGGACAGGGCTGAGGATGAGGAGAACCCTGGGGACCCAGAAGACCGTGCCTTGCCCGGAAGTCCTGCCTGTAGGCCT  
 GAAGGACTTGCCCTAACAGAGCCTCAACAACCTACCTGGTGATTCTTACTTCAGCCCCCTTGGTGTGAGCAGCTTCTCA  
 ACATGAAGTACAGCCTCCACTTGGCCTTCGTGTGTCTGAGTCTCTTCACTGAGAGGATGTGCATCCAGGGGAGTCAG  
 TTCAACGTCGAGGTCGGCAGAAGTGACAAGCTTTCCTGCCTGGCTTTGAGAACCTCACAGCAGGATATAACAAATT  
 TCTCAGGCCCAATTTTGGTGGAGAACCCGTACAGATAGCGCTGACTCTGGACATTGCAAGTATCTCTAGCATTTCAG  
 AGAGTAACATGGACTACACAGCCACCATATACCTCCGACAGCGCTGGATGGACCAGCGGCTGGTGTGTAAGGCAAC  
 AAGAGCTTCACTCTGGATGCCCCGCTCGTGGAGTTCTCTGGGTGCCAGATACTTACATTGTGGAGTCCAAGAAGTC  
 CTTCTCCATGAAGTCACTGTGGGAAACAGGCTCATCCGCCTCTTCTCCAATGGCACGGTCCTGTATGCCCTCAGAA  
 TCACGACAACCTGTTGCATGTAACATGGATCTGTCTAAATACCCCATGGACACACAGACATGCAAGTTGCAGCTGGAA  
 AGCTGGGGCTATGATGGAATGATGTGGAGTTCACCTGGCTGAGAGGGAACGACTCTGTGCGTGGACTGGAACACCT  
 GCGGCTTGCTCAGTACACCATAGAGCGGTATTTACCTTAGTCCAGATCGCAGCAGGAGACAGGAAATTACACTA  
 GATTGGTCTTACAGTTTGTAGCTTCGGAGGAATGTTCTGTATTTTCAATTTTGGAAACCTACGTTCTTCCACTTTCCTG  
 GTGGTGTGTCTCTGGGTTTTCATTTTGGATCTCTCTCGATTCACTCCCTGCAAGAACCTGCATTGGAGTGACGACCGT  
 GTTATCAATGACCACACTGATGATCGGTCCCACCTTCTCTTCCCAACACCAACTGCTTCATCAAGGCCATCGATG  
 TGTACCTGGGGATCTGCTTTAGCTTTGTGTTTGGGGCCTTGCTAGAAATATGCAGTTGCTCACTACAGTTCCTTACAG  
 CAGATGGCAGCCAAAGATAGGGGGACAACAAAGGAAGTAGAAGAAGTCAGTATTACTAATATCATCAACAGCTCCAT  
 CTCCAGCTTTAAACGGAAGATCAGCTTTGCCAGCATTGAAATTTCCAGCGACAACGTTGACTACAGTGACTTGACAA  
 TGAACACAGCGACAAGTTCAGTTCGCTTCCGAGAAAAGATGGGCAGGATTGTTGATTATTTTCACAATTCAAAAC  
 CCCAGTAATGTTGATCACTATTCCAACTACTGTTTCCTTTGATTTTTATGCTAGCCAATGTATTTTACTGGGCATA  
 CTACATGTATTTTTTGAAGTCAATGTTAAATTTCTTGCATGCCATAGGTCTTCAACAGGACAAGATAATGATGTAAATG  
 GTATTTTAGGCCAAGTGTGCACCCACATCCAATGGTGCTACAAGTGAATAATATTTGAGTCTTTCTGCTCAA  
 AGAATGAAGCTCCAACCATGTTCTAAGCTGTGTAGAAGTCTTAGCATTATAGGATCTTGTAATAGAAACATCAGTC  
 CATTCTCTTTTCACTTTAATCAAGGACATTCCCATGGAGCCCAAGATTACAAATGTACTCAGGGCTGTTTATTTCGGT  
 GGCTCCCTGGTTTGCATTTACCTCATATAAAGAATGGGAAGGAGACCATTGGGTAACCTCAAGTGTGAGAAGTTGT  
 TTCTAAAGTAACATACATGTTTTTTTACTAAATCTCTGCAGTGCTTATAAAATACATTGTTGCCTATTTAGGGAGTA  
 ACATTTTCTAGTTTTTGTCTGTTTAAATGAAATATGGGCTTATGTCAATTCATTGGAAGTCAATGCACTAACTC  
 AATACCAAGATGAGTTTTTAAATAATGAATATTATTTAATACCACAACAGAATTATCCCCAATTTCCAATAAGTCCT  
 ATCATTGAAAATTCAAATATAAGTGAAGAAAAAATTAGTAGATCAACAATCTAAACAAATCCCTCGGTTCTAAGATA  
 CAATGGATTCCCATACTGGAAGGACTCTGAGGCTTTATTTCCCCCACTATGCATATCTTATCATTTTATTATTATAC  
 ACACATCCATCCTAACTATACTAAAGCCCTTTTCCCATGCATGGATGGAAATGGAAGATTTTTTTGTAACCTGTTC  
 TAGAAGTCTTAATATGGGCTGTTGCCATGAAGGCTTGCAAGATTGAGTCCATTTTCTAGCTGCCTTTATTACATAG  
 TGATGGGGTACTAAAAGTACTGGGTTGACTCAGAGAGTCGCTGTCTATTCTGTCTATTGCTGCTACTTAACACTGAGC  
 AACACTCTCCAGTGGCAGATCCCTGTATCATTTCCAAGAGGAGCATTCATCCCTTTGCTCTAATGATCAGGAATGA  
 TGCTTATTAGAAAACAACTGCTTGACCCAGGAACAAGTGGCTTAGCTTAAGTAAACTTGGCTTTGCTCAGATCCCT  
 GATCCTTCCAGCTGGTCTGCTCTGAGTGGCTTATCCCGCATGAGCAGGAGCGTGTGGCCCTGAGTACTGAACCTTTC  
 TGAGTAACAATGAGACACGTACAGAACCTATGTTTCAGGTTGCGGGTGAGCTGCCCTCTCCAAATCCAGCCAGAGAT  
 GCACATTCCTCGGCCAGTCTCAGCCAACAGTACCAAAAGTGATTTTTTGTAGTGTGCCAGGGTAAAGGCTTCCAGTTCA  
 GCCTCAGTTATTTTAGACAATCTCGCCATCTTTAATTTCTTAGCTTCTGTTCTAATAAATGCACGGCTTTACCTTT  
 CCTGTGAGAAATAAACCAAGGCTCTAAAAGATGATTTCCCTTCTGTAACCTCCCTAGAGCCACAGGTTCTCATTCTT  
 TTCCCATTATACTTCTCACAATTCAGTTTCTATGAGTTTGATCACCTGATTTTTTTTAAACAAATATTTCTAACGGGA  
 ATGGGTGGGAGTGCTGGTGAAGAGATGAAATGTGGTTGTATGAGCCAATCATATTTGTGATTTTTTAAAAAAGT  
 TAAAAAGGAATATCTGTTCTGAAACCCCACTTAAGCATTGTTTTTATATAAAAAACAATGATAAAGATGTGAAGTGT  
 GAAATAAATATACCATATTAGCTACCCACCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 25**

TGCTGTCAGGGCGCTCAAGCTGCCGGGGAAGAAGAGCCAGACCTAGGGGAGTATGATCCACTTACCCAGGCTGACAGTGATGAGA  
 GCGAAGACGATCTGGTGTCTAACCTGCAGAAGAATGGAGGGGTCAAAATGGGAAGAGTCCTTTGGGAGAAGCGCCAGAACCCGAC  
 TCAGATGCTGAGGTTGCAGAGGCTGCAAAGCCACATCTTTCAGAACTCACCACGGAGGGCTACCCCTCAGAACCCCTTGGGGGCTC  
 GGAACAGAAGGCGGCCCTCCTCCCTGGTGTCTATGTGCGCACGCTGTCTTCTCTGCTGACTTTGGGGATCTCGATGATCTGGTGC  
 TCCTGTGTGCTTTCTGATCCCTGTCTCCAGAGATCTGCACAGCACCTGGAGCCGCCACTTTGGGCTCCCAGGGAGGTGGGGAC  
 CTGTCTCCATTGGAATTGGCTGATGTGAATGGAGATGGCTGCGTGATGTGCTTCTCTCTCTTTGTGATGTCAAGGAACGGGAGTGC  
 AGTAGGTGTCTCAAGACCAGCTGCTAATCTTGTGTGCTTTTCGGGGATGAATGGCAGCACACTGTGGTCTAGTCTTCTCCCTGAGG  
 AGGCTCGAGATATCACATGTTTGGAGCTGATGCCAGGAAGCTTTGGAAATGAAACCATCTGCCTTGTGACAGGGACACACAAGATGCTC  
 AGCGCATTCAATGCAACGTGAGGAAAGCCATTGGACTTTAAACCCAACTACTTGTCCAACGGTACCTTGGCTGCCCCAGTTGT  
 GGTACTGCCAGACTTGGATGAAGACGGTGTTCGAGACCTTGTGGTCTTGGCCATTGGGGAATTGACGCCAGATCTGTGCTTTCTGC  
 TGGTGTCTGGCCGGACCGAAATCCAGTGGGTGACCTGTGAAGTACAACATCGTTGGAGTTGGGAATCTGATTGGTCTCAGGTT  
 TACATCACCACAAAATGGGGCTGTCTACATCCTGTTTGGAGCTTTCAGGACACAGGATGAAAGATGATGGTTGTGGTGTGGTGC  
 CCAAATCGAGACAGCTCACCACCTTCTCTGCAGATAGAAGAGCCAGAATGGGAAAAGCGAAGATCCATCAACCTGTCTGAGCTCA  
 TTGATGTTTACAGTGATGGTGTGAACTACTCCAGATGGTGAAGGCACCAGATTCCAATGACGCAACCTTCTGATTACAACCAGA  
 CAAAGCTTGTGCTGCTTCGGGGGCAAAATCTGACACCTTACTGGGCATTGAGACTTCAAGGCTTGGCAGCCAGCCCTACTCTGG  
 ATATTTCACGTGATGATCAGACATTAGATTTCTTCTGCAGATCAGGATGGAGTTGGGATGAAAAGATGATGGTTGTGGTGTGGTGC  
 ACTCTGGCTCCATTGTTTGGAGTTACCGTGTCCGTGTACATGAAAGAAACGCCAGCCACCTCAGCAGTTACTTCAAGCCAGAAG  
 TCTGTCTTCTCTTCTGGGCCGAGGGCTGTGAGTGCATCTCCCAATTCGATATCATCTAGGAACTGAGCCGCCAGCCCTTCA  
 CCAGCTTTAGCTGATCCTGCTGCTTCCCTCCATCCTTCTGGATCTGGCCAACACCACCGGCACAGTGACGGCTTCAGAGGTTG  
 GAATTAACGACCTCTGGAAAGATGCTTTTATGTTTACAGGACAAAGGCCAAGCTCCGAAGGCCATCCAGCAGCCCTGGTGGTGC  
 AGCAAGCTTAGTCTACGGTGGGCACTAATGGAGGGCCAGATGGCTCAGCTACAGGAGTCCACCCCAAAATTTGGCCGTGGGGAGCT  
 GCGAAGATTTCTCTCTAGGATAAAGTTTGTGTAAGCTCCCTACGAGATCTAATCTGATGGAATCTTCAGTTGCAGAAGAAGTGAAC  
 AGAGTGGATACCCCTCTACTCTCTGTCACTGTAAATCAGTTCTATGGAGAGAAGACTTCTTCGTCTCATTACCACCTCCCT  
 GATGGTTGCAAAAGGCTTGGGAAGGCATGTTGGAGTCTTTGACGGCAGCATGATCTATTGGCTGGGGCATCTTACCTACCTTTTCA  
 GTCCCTGCATTAATCCCTCTAGGAATCTGCGTGGATCGTTTGGAAATGTGAATCTCTTAAGTATTTAATTTTTTGGTATGTCT  
 AATTTATGAAGTCTTGCTGGGAAAGCCAGTGAAGTCTATGACTAGGAAACATTTTGTGTACATTTGTGCTGTGTGTGTATATTT  
 TAGTGTGTGGTGAAGTTATTTTCCAGGTATGTCTAAGCTTCAGGATCCAGTTTCTTGTCTCTCTGAAATATATCTGGTTTGT  
 TGGTCATTTTGGAGCTTCCAGATGCCCTACCTCTGATGTTGAGGGCCACTTATTTCTCTCTTCTTCCACCTGTACCTTGG  
 CTACTTCCAATTTGTAGACAGAATGAGAAAGATTTATAGTGGAGACTGAGTTAGCCATCCAAGCATTTTCATCTCTCTTGTTTTA  
 TATCTTATTTCTTAGATTTTCCATCCATGTCTATTAAGTGACCACAAGAATAACTATATTTCTATCAAGGGGAGCAAGAGGAT  
 GTAGTCTCAGTGACCCATCTCTGACCAAGTCCACATGTTGTGTTATATGTGGCTCTGATGGTTCTGCCAGTCATGATCTTTTCT  
 GTGGCGACATCAGAAGTGATGTTTGCATGCTGTCTTCACTTAGAGGAGAAGTGGAAAGTCAAGGAGCTTGTATGCTCTATCTG  
 CTGATGTCTTCTCTGATCTTTTCTATAGGGCACCTCCTTAGCTCCCTCACTGTGTTTTCTTCTTCTATTAGGGATATGTTT  
 CTGGACTTTTTCTTCTGCTACTTGAGTCCAGGATGCAACCATTTTGTCTCTGATCTCTTCTTCTCTGTAGAGCCTTTGAAGCATG  
 TATTTTGGGAAAATTTCTGTAAATACTATAACTTTTATAAATGGTTAAGTTATTTAGAATTATCTCCAGTGCTTACTTCTCCCT  
 TCTTCTGTATAAATCTGCTACTTCAATTAAGTTCTCTCTAACTTTTAGGTCATTGTTTATATAGCAGAAAATTCATGTTAGCG  
 GATGGAAAATGCTTCTTGAATAACCTTGATAGGTCATCCCTGAGTGCACCTCAGGTTCTCTCTTTACCTGGGCTGTATCTTTTT  
 TTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTGTCTTGTGCGCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAC  
 CTTGCGCTCCTGGGTTCAAGCGATTCTCCAGCCTTAGCCTCCCAAGTAGCTGGGACTACAGGTGCCCGCTACCATGCCTGGCTAAT  
 TTTTTTTTTTGTATTTTGTAGTAGAGCGGGTTTACCATGTTGGCCAGGCTGGTCACGAACCTGACCTCAGATAATCCACCTG  
 CTTCTGCCTCCCAAAGTGTGGGATTACAGCGGTGAGCCACCATGCCCCGCTGGGCTGTATCTTTTAGCTTGTGTAGTAAAGG  
 ATTCTAGAAAATATGAAGTCCAGATTCAAAGGGATCTCTGTTAATTACCACTGACAGGCATTATGACCTAACAGGAGGTGGTA  
 GCAGTAGATCCAAGCATGCATGTTGCTGCGCTGTAGATTGGCCTTATCAGGTTTCTGGGTGCCTGTGCTTAAGATCCTGAAGGC  
 AAATTTTGTTCACAGTTTGGAAAGTCACTGTGGGTCCAGCTTGACTTTGGAGGAATAAGAAGATACTTCTAGAGTATGGGAATG  
 ATCCAGATAATTTCTGGGATTGAATCTACTTGAATTTAAGGGCCTGGGACCTAATTTGGTTTAGTATAGAATTTGAAGAATTAA  
 TTTATAGGCAGCTGAATACCAAACTTGGGTGGTGGTCTGTGGTTTGGCTGAGCTGTCCGGGCATAACCTGGTTCTCTGTTATG  
 TTAAGGCTTCTGGGAAGCCAGCCACTGCGCAGGAGTGAACATGAAGTTGTTTTCTGAGGACCTGTTTGGTGGGATTGTTT  
 GGCAGAGGACTGTGTTTATGCAGGGCAATCCCAGAAAGATAAGAGGAAGCTAGAGAACTTAATGTACCTGAATTTCTCATGGT  
 TATTTGCAAACTAATTAACATAGATTCTTTGACTATGGTAAGTTTGAATCTCTCTTGGCAACAACATTATAAGTTTGTAGTTT  
 CTTCTTCTCTTGCAGCCGCTACAGAAAGGTGTAAGTGGTGGCTGAAAATTGAGGAAGCTTCACTGACCAATGTGGGTGCTGGT  
 TCTTGTGAATGTGTCCCTAAGCCTCCTTCTCTTGCAGGCAGCCACCCACCCAGGTGTCTAAGATAGGACATGCTCCTTTCTTTC  
 TCTAATCCCATCCTGAGGTTGCCGGCAAAGCCAATATGACCACTACTGAGAAATAGTAATGACTTCTACAAATGCAAGGGTCTTAC  
 CCTCCTCTTCCCTTAAACACCTCCTTTCTTCTTACACCCGTTTTTGGCATCCCCCAAATGTGTGGTATGGTGAACATAATCCC  
 CTGAATGTGAATTGCTATCCTTATGCTTATTAAGAAGAGCCAGCTGGTATATTGTGAGGAGCACTATTTAAATGTGAAGT  
 TTATAGAGTAAATAAATAAATACTCTACAGG

**FIGURE 26**

**FIGURE 27**

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGGCTGGGCGCGCCCCC  
 GGGCCCCGCGCTGGGC**ATG**GGCGCACTGGCCCGGGCGCTGCTGCTGCCTCTGCTGGCCAGTGGCTCCTGCGCGCCG  
 CCCCCGAGCTGGCCCCCGCGCCCTTCACGCTGCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACC  
 CCGGGACCCGGGACCCCTGCCGAGCGCCACGCCAGCGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGC  
 GGGCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAGATGCTGA  
 TCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACCTTTGCCGTGGCAGGAACCCCGCAC  
 TCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTA  
 CACACAAGGAAGCTGGACGGGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTG  
 TCAACATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT  
 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAAGCAAACATCCCCAA  
 CGTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGG  
 GTGGAATTGAACCAAGTTTGTATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAA  
 ATTCTGAAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGA  
 CAGTGGCACCACGCTGCTGCGCTGCCCCAGAAGGTGTTTGATGCGGTGGTGAAGCTGTGGCCCGCGCATCTCTGA  
 TTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAATTCGGAACACCTTGGTCTTAC  
 TTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTA  
 CATTCAGCCCATGATGGGGGCCGGCCTGAATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCACAAATGCGCTGG  
 TGATCGGTGCCACGGTGATGGAGGGCTTCTACGTATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC  
 CCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTG  
 GTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCC  
 TCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGACGCTCGCCCCGTGACCCTGAGGTCGTCAATGAT  
 GAGTCCTCTCTGGTCAGACATCGCTGGAAAT**TGA**ATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAG  
 AAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTT  
 CTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAG  
 AAAAAATAATTAAAAAAAACCTTCATTCTAA

**FIGURE 28**

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGCTCTGGCAGGCTCCT  
GGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGGGCCTGGCCCAGCCAGCCTCTGCCCCGCCG  
GAAGCTGCTGGTGTTCTGCTGGATGGTTTTTCGCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTT  
TCAAAGAGATTGTGAGCAGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTAT  
TATACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACACATGTGGGACCCACCACCAACAA  
GTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAATGGATCAGAACCCTCTGTGGGTCACTC  
TGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACC  
TACTGCCTAGAATATAAAAATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAA  
GAGTGGCCGGGCCGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC  
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCCAGGAGCGGGGCCTG  
CAGGACCGCCTGAACGTCATTATTTTCTCGGATCACGGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCT  
GAATAAGTACATCAGCCTGAATGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTG  
GGAAACACTCTGAGATATATAACAAACTGAGCACAGTGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGC  
AGGTTCTATTACAAGAAAGGAAAGTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAACTGAGAA  
TCGAGAGATGCTTCCGTTTTTGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGCGTGATGGCACGGCTACGACA  
ACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATC  
AGGTCGGTGGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCGCTGCCCAACAACGGATCCTGGTCCAG  
GGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC  
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGC  
CAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATT  
CTTGATAATTCTATACATAAAAGTTCCTACTTGTAA

**FIGURE 29**

GCATTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGTACTCTTGGGAGTTTC  
CATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTGACACGTATCCAGCTACTGGTCCTGCTGATG  
ATGAAGCCCCTGATGCTGAAACCACTGCTGCTGCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCT  
GCTTCTACCACTGCTCGTAAAGACATTCCAGTTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCC  
CTGAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTCATGCTTCCTGTGATTTTCATCCAACACTTA  
CCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTCAAATAAAAAATAACTATGAGCAACATAAAA  
AAAAAAAAA

**FIGURE 30**

GACTACGGGGAGAGAGAGGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAAGAGCAAAGATGTTT  
CAAAC TGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGGCCCAGTTTGGAGGCCTGCCC GTGCCCT  
GGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTGCCCTTGAGTCCCACAGGTCTTGCAGGAAGCTTGACAAATG  
CCCTCAGCAATGGCCTGCTGTCTGGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCT  
GGAGGAGGTACTTCTGGTGGCCTCCTTGGGGGAÇTGCTTGGAAAAGTGACGTCAGTGATTCTGGCCTGAACAACAT  
CATTGACATAAAGGTCACTGACCCCCAGCTGCTGGAACCTTGGCCTTGTGCAGAGCCCTGATGGCCACCGTCTCTATG  
TCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCTGGTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAG  
CTGGACATCACTGCAGAAATCTTAGCTGTGAGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGA CTGACCCA  
TTCCCTGGAAGCCTGCAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCA  
CAGGGATCTTGAATAAAGTCTGCCTGAGTTGGTTCAGGGCAACGTGTGCCCTCTGGTCAATGAGGTTCTCAGAGGC  
TTGGACATCACCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTACAGTTTGT CATCAAGGTCTAAGCCTT  
CCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAGTGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACA  
GTTGCCTTCTCTCCGAGGAACCTGCCCCCTCTCCTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAAT  
AAAATGGCTCTTCTTATGCA

**FIGURE 31**

GGGCGCTGGGAGACACCGGACGCCCCGCTCGGCTGCGCTGCGGGCTCAGGCCCCCGCTCGGGCCCCGACCCGCTCGGTCA  
 CCGCCGGCTCGGGCGCGCACCTGCCGGCTGCGGGCCCCAGGGCCATGCGGAGGCCCCACGAGGAGGCCGGCGGCCACGC  
 GCATCCCGTAGCCAGGTGGCCAGGTCTGCACCGCGGGCGGCCTCGGCGCC**ATGG**AGCCCCCGTATTCTGCTGACGGC  
 GCACTACGATGAGTTCCAAGAGGTCAAGTACGTGAGCCGCTGCGGCGCGGGGGGCGCGCGGGGGCCTCCCTGCCCC  
 CGGGCTTCCCGTTGGGCGCTGCGCGCAGCGTCACCGGGGCCCGGTCCGGGCTGCCGCGCTGGAACCGGCGCGAGGTG  
 TGCCTGCTGTCGGGGCTGGTGTTCGCCGCCGGCCTCTGCGCCATTCTGGCGGCTATGCTGGCCCTCAAGTACCTGGG  
 CCGGTGCGGGCCGGCGGGCGGCCCTGTCCGAGGGCTGCCCTGAGCGCAAGGCCCTTCGCGCGCGCCGCTCGCTTCC  
 TGGCCGCCAACCTGGACGCCAGCATCGACCCATGCCAGGACTTCTACTCGTTTCGCTGCGGGCGGTTGGCTGCGGCGC  
 CACGCCATCCCCGACGACAAGCTCACCTATGGCACCATCGCGGCCATCGGCGAGCAAAACGAGGAGCGCCTACGGCG  
 CCTGCTGGCGCGGCCCGGGGTGGCCCTGGCGGCGCGGCCAGCGCAAGGTGCGCGCCTTCTTCGCTCGTGCCTCG  
 ACATGCGCGAGATCGAGCGACTGGGCCCGCGACCCATGCTAGAGGTATCGAGGACTGCGGGGGCTGGGACCTGGGC  
 GCGCGGAGGAGCGTCCGGGGGTGCGGCGCGATGGGACCTCAACCGGCTGCTGTACAAGGCGCAGGGCGTGTACAG  
 CGCCGCCGCTCTTCTCGCTCACGGTCAGCCTGGACGACAGGAACCTCTCGCGCTACGTATCCGCATTGACCAGG  
 ATGGGCTCACCTGCCAGAGAGGACCTGTACCTCGCTCAGGATGAGGACAGTGAGAAGATCCTGGCAGCATACAGG  
 GTGTTATGGAGCGAGTGCTCAGCCTCCTGGGTGCAGACGCTGTGGAACAGAAGGCCCAAGAGATCCTGCAAGTGGA  
 GCAGCAGCTGGCCAACATCACTGTGTACAGATATGACGACCTACGCGGAGATGTACGCTCCATGTACAACAAGGTGA  
 CGCTGGGGCAGCTGCAGAAGATCACCCCCACTTGCGGTGGAAGTGGCTGCTAGACCAGATCTTCCAGGAGGACTTC  
 TCAGAGGAAGAGGAGGTGGTGTCTGTCGCGACAGACTACATGCAGCAGGTGTGCGAGCTCATCCGCTCCACACCCCA  
 CCGGGTCTTGCACAACTACCTGGTGTGGCGCGTGGTGGTGGTCTGAGTGAACACCTGTCCCCGCCATTCCGTGAGG  
 CACTGCACGAGCTGGCACAGGAGATGGAGGGCAGCGACAAGCCACAGGAGCTGGCCCCGGTCTGCTTGGGCCAGGCC  
 AATCGCCACTTTGGCATGGCGCTTGGCGCCCTCTTGTACATGAGCACTTCTCAGCCGCCAGCAAAGCCAAGGTGCA  
 GCAGCTAGTGAAGACATCAAGTACATCCTGGGCCAGCGCCTGGAGGAGCTGGACTGGATGGACGCCGAGACCAGGG  
 CTGCTGCTCGGGCCAAGCTCCAGTACATGATGGTGTATGGTTCGGCTACCCGGACTTCTGCTGAAACCCGATGCTGTG  
 GACAAGGAGTATGAGTTTGGGTCCATGAGAAGACCTACTTCAAGAACATCTTGAACAGCATCCCCCTTCAGCATCCA  
 GCTCTCAGTTAAGAAGATTCCGGCAGGAGGTGGACAAGTCCACGTGGCTGCTCCCCCCACAGGCGCTCAATGCCTACT  
 ATCTACCCAACAAGAACCAGATGGTGTTCGCCGCGGCATCCTGCAGCCACCCTGTACGACCCCTGACTTCCCACAG  
 TCTCTCAACTACGGGGGCATCGGCACCATCATTTGGACATGAGCTGACCCACGGCTACGACGACTGGGGGGGCCAGTA  
 TGACCGCTCAGGGAACCTGCTGCACTGGTGGACGGAGGCCTCCTACAGCCGCTTCTGCGAAAGGCTGAGTGCATCG  
 TCCGTCTCTATGACAACTTCACTGTCTACAACCAGCGGGTGAACGGGAAACACACGCTTGGGGAGAACATCGCAGAT  
 ATGGGCGTCTCAAGCTGGCCTACCACGCCTATCAGAAGTGGGTGCGGGAGCACGGCCAGAGACCCACTTCCCCG  
 GCTCAAGTACACATGACCAGCTCTTCTTCAATTGCCTTTGCCCAGAACTGGTGCATCAAGCGGCGGTGCGAGTCCA  
 TCTACCTGCAGGTGCTGACTGACAAGCATGCCCCTGAGCACTACAGGGTGTGGGCGAGTGTGTCCAGTTTGAGGAG  
 TTTGGCCGGGCTTTCCACTGTCCCAAGGACTCACCCATGAACCTGCCACAAGTGTTCGTGTGG**TGA**CGCCTGGCT  
 GCGCGCTGCACGCCCCCACTGCCCCCGCACGAATCACCTCCTGCTGGCTACCGGGGCAGGCATGCACCCGGTGCCA  
 GCCCCGCTTGGGCACCACCTGCCTTCCAGCCCCCTCCAGGACCCGGTCCCCCTGCTGCCCCCTCACTTCAGGAGGGGC  
 CTGGAGCAGGGTGAGGCTGGACTTTGGGGGGCTGTGAGGGAAATATACTGGGGTCCCCAGATTCTGCTCTAAGGGGG  
 CCAGACCCTCTGCCAGGCTGGATTGTACGGGCCCCACCTTCGCTGTGTTCTTGCTGCAAAGTCTGGTCAATAAATCA  
 CTGCACTGTTAAAAA



**FIGURE 32**

GAGAGAACAGCGTGAGCCTGTGTGCTTGTGTGCTGAGCCCTCATCCCCCTCCTGGGGCCAGGCTTGGGTTTACCTGC  
 AGAATCGCTTGTGCTGGGCTGCCTGGGCTGTCTCAGTGGCACCTGCATGAAGCCGTTCTGGCTGCCAGAGCTGGAC  
 AGCCCCAGGAAAACCCACCTCTCTGCAGAGCTTGCCAGCTGTCCCCGGAAGCCAAATGCCTCTCATGTAAGTCTT  
 CTGCTCGACGGGGTGTCTCCTAAACCCTCACTCTTCAGCCTCTGTTTGACCATGAAATGAAGTGACTGAGCTCTATT  
 CTGTACCTGCCACTCTATTTCTGGGGTGACTTTTGTGACGTGCCCAGAATCTCCAAGCCAGGCTGGTTCTCTGCATC  
 CTTTCAATGACCTGTTTTCTTCTGTAAACCACAGGTTCCGGTGGTGAGAGGAAGCCTCGCAGAATCCAGCAGAATCCTC  
 ACAGAATCCAGCAGCAGCTCTGCTGGGGACATGGTCCATGGTGCAACCCACAGCAAAGCCCTGACCTGACCTCCTGA  
 TGCTCAGGAGAAGCCCATGGGGCCCCTCCTGTCTGTGTTCTGTCTTCACAAAGCTCAGCCTGTGGTGCTCCTTCT  
 GACCCCAGCAGGTGGAGAGGAAGCTAAGCGCCCACCTCCCAGGGCTCCTGGAGACCCACTCTCCTCTCCAGTCCCA  
 CGGCATTGCCGCAGGGAGGCTCGCATACCGAGACTGAGGACCGGCTCTTCAAACACCTCTTCCGGGGCTACAACCGC  
 TGGGCGCGCCCGGTGCCAACACTTCAGACGTGGTGATTGTGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT  
 GGATGAGAAGAACCAAATGATGACCACCAACGTCTGGCTAAAACAGGAGTGGAGCGACTACAACTGCGCTGGAACC  
 CCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGAGATGATCTGGATCCCCGACATTGTTCTCTACAAC  
 AATGCAGATGGGGAGTTTGCAGTGACCCACATGACCAAGGCCACCTCTTCTCCACGGGCACGTGCACTGGGTGCC  
 CCGGCCATCTACAAGAGCTCCTGCAGCATCGACGTACCTTCTTCCCCTTCGACCAGCAGAAGTGAAGATGAAGT  
 TTGGCTCCTGGACTTATGACAAGGCCAAGATCGACCTGGAGCAGATGGAGCAGACTGTGGACCTGAAGGACTACTGG  
 GAGAGCGGCGAGTGGGCCATCGTCAATGCCACGGGCACCTACAACAGCAAGAAGTACGACTGCTGCGCCGAGATCTA  
 CCCCAGCTCACCTACGCCCTTCGTATCCGGGGCTGCCGCTCTTCTACACCATCAACCTCATCATCCCCGCTGCCTGC  
 TCATCTCCTGCCTCACTGTGCTGGTCTTCTACCTGCCCTCCGACTGCGGCGAGAAGATCACGCTGTGCATTTCCGGT  
 CTGCTGTCACTACCGTCTTCCTGTGCTCATCACTGAGATCATCCCGTCCACCTCGCTGGTCATCCCGCTCATCGG  
 CGAGTACCTGCTGTTACCATGATCTTCGTACCCCTGTCCATCGTCATCACCGTCTTCGTGCTCAATGTGCACCACC  
 GCTCCCCCAGCACCCACACCATGCCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCGGTGGCTTCTGATG  
 AACCGGGCCCCACCACCCGTGGAGCTCTGCCACCCCTACGCCTGAAGCTCAGCCCTCTTATCACTGGCTGGAGAG  
 CAACGTGGATGCCGAGGAGAGGGAGGTGGTGGTGGAGGAGGAGGACAGATGGGCATGTGCAGGTCATGTGGCCCCCT  
 CTGTGGGCACCCTCTGCAGCCACGGCCACCTGCACTCTGGGGCCTCAGGTCCCAAGGCTGAGGCTCTGCTGCAGGAG  
 GGTGAGCTGCTGCTATACCCACATGCAGAAGGCACTGGAAGGTGTGCACTACATTGCCGACCACCTGCGGTCTGA  
 GGATGCTGACTCTTCGGTGAAGGAGGACTGGAAGTATGTTGCCATGGTCATCGACAGGATCTTCCTCTGGCTGTTTA  
 TCATCGTCTGCTTCCTGGGGACCATCGGCCTCTTCTGCCTCCGTTCCCTAGCTGGAATGATCTGACTGCACCTCCCT  
 CGAGCTGGCTCCCAGGGCAAAGGGGAGGGTTCTTGATGTGGAAGGGCTTTGAACAATGTTTAGATTTGGAGATGAG  
 CCCAAAGTGCCAGGGAGAACAGCCAGGTGAGGTGGGAGGTGGAGAGCCAGGTGAGGTCTCTCTAAGTCAGGCTGGG  
 GTTGAAGTTTGGAGTCTGTCCGAGTTTGCAGGTGCTGAGCTGTATGGTCCAGCAGGGGAGTAATAAGGGCTCTTCC  
 GGAAGGGGAGGAAGCGGGAGGCAGGCCTGCACCTGATGTGGAGGTACAGGCAGATCTTCCCTACCGGGGAGGGATGG  
 ATGGTTGGATACAGGTGGCTGGGCTATTCCATCCATCTGGAAGCACATTTGAGCCTCCAGGCTTCTCCTTGACGTCA  
 TTCCTCTCCTTCTTGCTGCAAAATGGCTCTGCACCAGCCGGCCCCCAGGAGGTCTGGCAGAGCTGAGAGCCATGGC  
 CTGCAGGGGCTCCATATGTCCCTACGCGTGACAGGCAACAAGA

**FIGURE 33**

CTCTGTCCTGGGACTTGGTGGTGCTACCCTTGGCCTCCACAGTCCTGCCACCCTGCTGCCGCCACCATGCTGCCCC  
CTGGGACTGCGACCCTCTTGACTCTGCTCCTGGCAGCTGGCTCGCTGGGCCAGAAGCCTCAGAGGCCACGCCGGCCC  
GCATCCCCCATCAGCACCATCCAGCCCAAGGCCAATTTTGATGCTCAGCAGTTTGCAGGGACCTGGCTCCTTGTGGC  
TGTGGGCTCCGCTTGCCGTTTCTGTCAGGAGCAGGGCCACCGGGCCGAGGCCACCACACTGCATGTGGCTCCCCAGG  
GCACAGCCATGGCTGTCAGTACCTTCCGAAAGCTGGATGGGATCTGCTGGCAGGTGCGCCAGCTCTATGGAGACACA  
GGGGTCCTCGGCCGCTTCTGCTTCAAGCCCAGGCGCCCGAGGGGCTGTGAACGTGGTTGTCGCTGAGACTGACTA  
CCAGAGTTTCGCTGTCCTGTACCTGGAGCGGGCGGGGCAGCTGTCAGTGAAGCTCTACGCCCGCTCGCTCCCTGTGA  
GCGACTCGGTCTGAGTGGGTTTGAGCAGCGGGTCCAGGAGGCCACCTGACTGAGGACCAGATCTTCTACTTCCCC  
AAGTACGGCTTCTGCGAGGCTGCAGACCAGTTCCACGTCCTGGACGAAGTGAGGAGGTGAGGCCGGCACACAGCTCC  
AGTGCTGAGAAGTCAGTGCCCCGAGAGACGACCCACCAAGTGGGGTGCCCGCTGCCTGTCTCCGTGAAACCAGCCT  
CAGATCAGGGCCCTGCCACCCAGGGCAGGGGATCTTCTGCCGGCTGCCCCAGAGGACAGTGGGTGGAGTGGTACCTA  
CTTATTAAATGTCTCAGACCCCAAAAAAAAAAAAAAAAAA

**FIGURE 34**

AAGAACAATTGTCTCTGGACGGCAGCT**ATG**CGACTCACCGTGCTGTGTGCTGTGTGCCTGCTGCCTGGCAGCCTGGC  
CCTGCCGCTGCCTCAGGAGGCGGGAGGCATGAGTGAGCTACAGTGGGAACAGGCTCAGGACTATCTCAAGAGATTTT  
ATCTCTATGACTCAGAAACAAAAATGCCAACAGTTTAGAAGCCAAACTCAAGGAGATGCAAAAATCTTTGGCCTA  
CCTATAACTGGAATGTTAAACTCCCGCGTCATAGAAATAATGCAGAAGCCCAGATGTGGAGTGCCAGATGTTGCAGA  
ATACTCACTATTTCCAAATAGCCCAAAATGGACTTCCAAAGTGGTCACCTACAGGATCGTATCATATACTCGAGACT  
TACCGCATATTACAGTGGATCGATTAGTGTCAAAGGCTTTAAACATGTGGGGCAAAGAGATCCCCCTGCATTTCAGG  
AAAGTTGTATGGGGAAGTCTGACATCATGATTGGCTTTGCGCGAGGAGCTCATGGGGACTCCTACCCATTTGATGG  
GCCAGGAAACACGCTGGCTCATGCCTTTGCGCCTGGGACAGGTCTCGGAGGAGATGCTCACTTCGATGAGGATGAAC  
GCTGGACGGATGGTAGCAGTCTAGGGATTAACTTCCTGTATGCTGCAACTCATGAAC TTGGCCATTCTTTGGGTATG  
GGACATTCCTCTGATCCTAATGCAGTGATGTATCCAACCTATGGAAATGGAGATCCCCAAAATTTTAAACTTTCCCA  
GGATGATATTAAAGGCATTCAGAACTATATGGAAAGAGAAGTAATTCAAGAAAGAAA**TAG**AAACTTCAGGCAGAAC  
ATCCATTCATTCATTCATTGGATTGTATATCATTTGTTGCACAATCAGAATTGATAAGCACTGTTCCCTCCACTCCATT  
TAGCAATTATGTCACCCCTTTTTTATTGCAGTTGGTTTTTGAATGTCTTTCACTCCTTTTATTGGTTAAACTCCTTTA  
TGGTGTGACTGTGTCTTATTCCATCTATGAGCTTTGTCACTGCGCGTAGATGTCAATAAATGTTACATACACAAATA  
AATAAAATATTTAGGCCATGGTAAATTTACC

**FIGURE 35**

GAGCGAGCACCTTCGACGCGGTCCGGGGACCCCTCGTCGCTGTCTCCCGACGCGGACCCGCGTGCCCCAGGCCTC  
GCGCTGCCCCGGCCGGCTCCTCGTGTCCCACTCCCGGCGCACGCCCTCCCGCGCCCTCTTCTCGGCGCGCGCAGC  
**ATG**GCGCCCCCGCAGGTCCCTCGCGTTTCGGGCTTCTGCTTGCCGCGGCGACGGCGACTTTTGCCGCAGCTCAGGAAGA  
ATGTGTCTGTGAAAATAACAAGCTGGCCGTAAACTGCTTTGTGAATAATAATCGTCAATGCCAGTGTACTTCAGTTG  
GTGCACAAAATACTGTCATTTGCTCAAAGCTGGCTGCCAAATGTTTGGTGATGAAGGCAGAAATGAATGGCTCAAAA  
CTTGGGAGAAGAGCAAAACCTGAAGGGGCCCTCCAGAACAATGATGGGCTTTATGATCCTGACTGCGATGAGAGCGG  
GCTCTTTAAGGCCAAGCAGTGCAACGGCACCTCCACGTGCTGGTGTGTGAACACTGCTGGGGTCAGAAGAACAGACA  
AGGACACTGAAATAACCTGCTCTGAGCGAGTGAGAACCTACTGGATCATCATTGAACTAAAACACAAAGCAAGAGAA  
AAACCTTATGATAGTAAAAGTTTGCGGACTGCACTTCAGAAGGAGATCACACGCGTTATCAACTGGATCCAAAATT  
TATCACGAGTATTTTGTATGAGAATAATGTTATCACTATTGATCTGGTTCAAATTTCTTCTCAAAAAACTCAGAATG  
ATGTGGACATAGCTGATGTGGCTTATTATTTTGAAAAAGATGTTAAAGGTGAATCCTTGTTTCATTCTAAGAAAATG  
GACCTGACAGTAAATGGGGAACAACCTGGATCTGGATCCTGGTCAAACTTTAATTTATTATGTTGATGAAAAAGCACC  
TGAATTCTCAATGCAGGGTCTAAAAGCTGGTGTATTGCTGTTATTGTGGTTGTGGTGATGGCAGTTGTTGCTGGAA  
TTGTTGTGCTGGTTATTTCCAGAAAGAAGAGAATGGCAAAGTATGAGAAGGCTGAGATAAAGGAGATGGGTGAGATG  
CATAGGGAACCTCAATGCAT**TAA**CTATATAATTTGAAGATTATAGAAGAAGGGAAATAGCAAATGGACACAAATTACAA  
ATGTGTGTGCGTGGGACGAAGACATCTTTGAAGGTCATGAGTTTGTAGTTTAACATCATATATTTGTAATAGTGAA  
ACCTGTACTCAAAATATAAGCAGCTTGAACTGGCTTTACCAATCTTGAAATTTGACCACAAGTGTCTTATATATGC  
AGATCTAATGTAAATCCAGAACTTGGACTCCATCGTTAAATTTATTTATGTGTAACATTCAAATGTGTGCATTAAA  
TATGCTTCCACAGTAAAATCTGAAAACTGATTTGTGATTGAAAGCTGCCTTTCTATTTACTTGAGTCTTGACATA  
CATACTTTTTTATGAGCTATGAAATAAAACATTTTAAACTG

GCTCCGGGCTGAAGATTGCTTCTCTTCTCTCCTCCAAGGTCTAGTGACGGAGCCCCGCGCGCGCCACCATGCGGCA  
GAAGGCGGTATCCGTTTTCTGTGCTACCTGCTGCTCTTCACTTGCAGTGCGGTGGAGGCAGGTAAGAAAAAGTGCT  
CGGAGAGCTCGGACAGCGGCTCCGGGTTCTGGAAGGCCCTGACCTTCATGGCCGTCGGAGGAGGACTCGCAGTCGCC  
GGGTGCCCCGCGCTGGGCTTACCGGCGCCGGCATCGCGGCCAACTCGGTGGCTGCCTCGCTGATGAGCTGGTCTGC  
GATCCTGAATGGGGGCGCGTGCCCGCCGGGGGGCTAGTGCCACGCTGCAGAGCCTCGGGGCTGGTGGCAGCAGCG  
TCGTCATAGGTAATATTGGTGCCCTGATGCGGTACGCCACCCACAAGTATCTCGATAGTGAGGAGGATGAGGAGTAC  
CCAGCAGCTCCCAGAACCTCTTCTTCTTCTTGGCCTAACTCTTCCAGTTAGGATCTAGAACTTTGCCTTTTTTTTT  
TTTTTTTTTTTTTTGAGATGGGTTCTCACTATATTGTCCAGGCTAGAGTGCACTGGCTATTACAGATGCCAACATA  
GTAACTGTCAGCCTCCAACTCCTAGCCTCAAGTGATCCTCCTGTCTCAACCTCCCAAGTAGGATTACAAGCATGCGC  
CGACGATGCCAGAATCCAGAACTTTGTCTATCACTCTCCCCAACACCTAGATGTGAAAACAGAATAAACTTCACC  
CAGAAAA

**FIGURE 37**

GCCGCCGAGGGCAGCCAGCCCCCTCCCTACCCGGAGCAGCCCGCTGGGGCCGTCCCGAGCGGCGACACACTAGGAGT  
 CCCGGCCGGCCAGCCAGGGCAGCCCGGTCCCGGGACTCGGCCGTGAGTGCTGCGGGACGGATGGTGGCGGCGGGAG  
 CGCGGAGACCACGGCGGGCGCCGTGGAGCCGGCGCCGTGCAGCCGGAGCTGCGCGCGGGGGCATGCGGCTGCGCCCC  
 GGCCCCCTCGGCCCCCGGCTCGGCCCCCGCGCTCCGGCCCCAGCCCCGGCCGCGCGGGCCCCCGGGAGTGACGCGACC  
 GCGCCGCGCTGAGGGAGGCGCCCCACC**ATG**CCGCGGGCCCCGGCGCCGTGTACGCCTGCCTCCTGGGGCTCTGCG  
 CGCTCCTGCCCCGGCTCGCAGGTCTCAACATATGCACTAGTGGAAGTGCCACCTCATGTGAAGAATGTCTGCTAATC  
 CACCCAAAATGTGCCTGGTGCTCCAAAGAGGACTTCGGAAGCCCACGGTCCATCACCTCTCGGTGTGATCTGAGGGC  
 AAACCTTGTCAAAAATGGCTGTGGAGGTGAGATAGAGAGCCCAGCCAGCAGCTTCCATGTCTGAGGAGCCTGCCCC  
 TCAGCAGCAAGGGTTCGGGCTCTGCAGGCTGGGACGTATTAGATGACACCACAGGAGATTGCCGTGAACCTCCGG  
 CCCGGTGACAAGACCACCTTCCAGCTACAGGTTCCGACAGGTGGAGGACTATCCTGTGGACCTGTACTACCTGATGGA  
 CCTCTCCCTGTCCATGAAGGATGACTTGGACAATATCCGGAGCCTGGGCACCAAACTCGCGGAGGAGATGAGGAAGC  
 TCACCAGCAACTTCCGGTTGGGATTTGGGTCTTTTGTGTGATAAGGACATCTCTCCTTTCTCCTACACGGCACCGAGG  
 TACCAGACCAATCCGTGCATTGGTTACAAGTTGTTTCAAATTGCGTCCCCCTCCTTTGGGTTCGCCATCTGCTGCC  
 TCTCACAGACAGAGTGACAGCTTCAATGAGGAAGTTCGGAAACAGAGGGTGTCCCGGAACCGAGATGCCCTGAGG  
 GGGGCTTTGATGCAGTACTCCAGGCAGCCGTCTGCAAGGAGAAGATTGGCTGGCGAAAGGATGCACTGCATTTGCTG  
 GTGTTCAACAAGATGATGTGCCCCACATCGCATTGGATGGAAAAATTGGGAGGCCTGGTGCAGCCACACGATGGCCA  
 GTGCCACCTGAACGAGGCCAACGAGTACACAGCATCCAACCAGATGGACTATCCATCCCTTGCTTGGAGAGA  
 AATTGGCAGAGAACAACATCAACCTCATCTTTGCAGTGACAAAAAACCATTTATATGCTGTACAAGAATTTTACAGCC  
 CTGATACCTGGAACAACGTGGAGATTTTAGATGGAGACTCCAAAAATATTATCAACTGATTATTAATGCATACAA  
 TAGTATCCGGTCTAAAGTGGAGTTGTGAGTCTGGGATCAGCCTGAGGATCTTAATCTCTTTTACTGCTACCTGCC  
 AAGATGGGGTATCCTATCCTGGTCAGAGGAAGTGTGAGGGTCTGAAGATTGGGGACACGGCATCTTTTGAAGTATCA  
 TTGGAGGCCCGAAGCTGTCCAGCAGACACACGGAGCATGTGTTTGGCTGCGGCCGGTGGGATTCCGGGACAGCCT  
 GGAGGTGGGGGTACCTACAACCTGCACGTGCGGCTGCAGCGTGGGGCTGGAACCCAACAGCGCCAGGTGCAACGGGA  
 GCGGGACCTATGTCTGCGGCCTGTGTGAGTGACGCCCCGGCTACCTGGGCACCAGGTGCGAGTGCCAGGATGGGGAG  
 AACCAGAGCGTGTACCAGAACCTGTGCCGGGAGGCGAGGGCAAGCCACTGTGCAGCGGGCGTGGGGACTGCAGCTG  
 CAACCAGTGCTCCTGCTTCGAGAGCGAGTTTGGCAAGATCTATGGGCCTTTCTGTGAGTGCGACAACCTCTCCTGTG  
 CCAGGAACAAGGGAGTCTCTGTCTCAGGCCATGGCGAGTGTCACTGCGGGGAATGCAAGTGCCATGCAGGTTACATC  
 GGGGACAACCTGTAACGTCTCGACAGACATCAGCACATGCCGGGCGAGAGATGGCCAGATCTGCAGCGAGCGTGGGCA  
 CTGTCTCTGTGGGCAGTGCCAATGCACGGAGCCGGGGGCTTTGGGGAGATGTGTGAGAAGTGCCCCACCTGCCCGG  
 ATGCATGCAGCACCAGAGAGATTGCGTCGAGTGCCCTGCTGCTCCACTCTGGGAAACCTGACAACCAGACCTGCCAC  
 AGCCTATGCAGGGATGAGGTGATCACATGGGTGGACACCATCGTGAAAGATGACCAGGAGGCTGTGCTATGTTTCTA  
 CAAAACCGCCAAGGACTGCGTCATGATGTTACCTATGTGGAGCTCCCAGTGGAAGTCCAACCTGACCGTCTCTCA  
 GGGAGCCAGAGTGTGGAAACACCCCCAACGCCATGACCATCCTCCTGGCTGTGGTGGTGGTGGTGGTGGTGGTGGT  
 CTTGCACTCCTGGCTATCTGGAAGCTGCTTGTACCATCCACGACCGGAGGGAGTTTGCAAAGTTTTCAGAGCGAGCG  
 ATCCAGGGCCCGCTATGAAATGGCTTCAAATCCATTATACAGAAAGCCTATCTCCACGCACACTGTGGACTTCACCT  
 TCAACAAGTTCAACAAATCCTACAATGGCACTGTGGACT**TGA**TGTTTCCTTCTCCGAGGGGCTGGAGCGGGGATCTGA  
 TGAAGAGTTCAGACTGAAACGCCTTGACGGCTGCTCGGCTTGATCACAGCTCCCTAGGTAGGCACCACAGAGAAGA  
 CTTTCTAGTGAGCCTGGGCCAGGAGCCACAGTGCTGTACAACAAGGGAAGGTAGCCTGGCCATGTACCTGGCTG  
 CTAGCCAGAGCCATGCCAGGTTGCGCTCCCTAAGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTTCC  
 CTGCCACATCCAGCTTGTGTCCCAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTTCCAGGAATCGTGGGCCCC  
 CAGCCTGGCCAGACAAGAAGACTGTGAGGAAGGGTCGGAGTCTGTAAAACCAGCATACAGTTTGGCTTTTTTTCACAT  
 TGATCATTTTTATATGAAATAAAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCCTGAGACTTTTCTGCGTGATGC  
 TATGCCTTGACACAGGTGTTGGTGATGGGGCTGTTGAGATGCCTGTTGAAGGTACATCGTTTGCAAATGTCAGTTT  
 CCTCTCCTGTCCGTGTTTGTGTTAGTACTTTTATAATGAAAAGAAACAAGATTGTTTGGGATTGGAAGTAAAGATTAA  
 AACCAAAAGAATTTGTGTTTGTCTGCCC

**FIGURE 38**

CGACTCACTATAGGGCGAATTGAATTTAGCGGCCGCGAATTCGCCCTT**ATG**CTGCCACAAATACCCTTTTGGCTGCT  
 AGTATCCTTGAACCTTGGTTCATGGAGTGTTTTACGCTGAACGATACCAAATGCCCACAGGCATAAAAGGCCACTAC  
 CCAACACCAAGACACAGTTCTTCATTCCCTACACCATAAAGAGTAAAGGTATAGCAGTAAGAGGAGAGCAAGGTACT  
 CCTGGTCCACCAGGCCCTGCTGGACCTCGAGGGCACCAGGTCTTCTGGACCACCAGGAAAACCAGGCTACGGAAG  
 TCCTGGACTCCAAGGAGAGCCAGGGTTGCCAGGACCACGGGACCATCAGCTGTAGGGAAACCAGGTGTGCCAGGAC  
 TCCCAGGAAAACCAGGAGAGAGAGGACCATATGGACCAAAGGAGATGTTGGACCAGCTGGCCTACCAGGACCCCGG  
 GGCCACCAGGACCACCTGGAATCCCTGGACCGGCTGGAATTTCTGTGCCAGGAAAACCTGGACAACAGGGACCCAC  
 AGGAGCCCCAGGACCCAGGGGCTTTCTGGAGAAAAGGGTGCAACCAGGAGTCCCTGGTATGAATGGACAGAAAGGGG  
 AAATGGGATATGGTGCTCCTGGTCGTCCAGGTGAGAGGGGTCTTCCAGGCCCTCAGGGTCCCACAGGACCATCTGGC  
 CCTCCTGGAGTGGGAAAAAGAGGTGAAAATGGGGTTCCAGGACAGCCAGGCATCAAAGGTGATAGAGGTTTTCCGGG  
 AGAAATGGGACCAATTGGCCCACCAGGTCCCCAAGGCCCTCCTGGGGAACGAGGGCCAGAAGGCATTGGAAAGCCAG  
 GAGCTGCTGGAGCCCCAGGCCAGCCAGGGATTCCAGGAACAAAAGGTCTCCCTGGGGCTCCAGGAATAGCTGGGCCC  
 CCAGGGCCTCCTGGCTTTGGGAAACCAGGCTTGCCAGGCCTGAAGGGAGAAAGAGGACCTGCTGGCCTTCTGGGGG  
 TCCAGGTGCCAAAGGGGAACAAGGGCCAGCAGGTCTTCCCTGGGAAGCCAGGTCTGACTGGACCCCTGGGAATATGG  
 GACCCCAAGGACCAAAAGGCATCCCGGGTAGCCATGGTCTCCAGGCCCTAAAGGTGAGACAGGGCCAGCTGGGCCT  
 GCAGGATACCTGGGGCTAAGGGTGAAAGGGGTCCCTGCGGTGAGTGGAAAACCAGGGTACCCAGGAAAACCAGG  
 TCTCGATGGTCCTAAGGGTAACCCAGGGTTACCAGGTCCAAAAGGTGATCCTGGAGTTGGAGGACCTCCTGGTCTCC  
 CAGGCCCTGTGGGGCCAGCAGGAGCAAAGGGAATGCCGGACACAATGGAGAGGCTGGCCCAAGAGGTGCCCCTGGA  
 ATACCAGGTACTAGAGGCCCTATTGGGCCACCAGGCATTCCAGGATTCCCTGGGTCTAAAGGGGATCCAGGAAGTCC  
 CGGTCTCCTGGCCCAGCTGGCATAGCAACTAAGGGCCTCAATGGACCCACCGGGCCACCAGGGCCTCCAGGTCCAA  
 GAGGCCACTCTGGAGAGCCTGGTCTTCCAGGGCCCCCTGGGCCTCCAGGCCACCAGGTCAAGCAGTCATGCCTGAG  
 GGTTTTATAAAGGCAGGCCAAAGGCCAGTCTTTCTGGGACCCCTCTTGTTAGTGCCAACCAGGGGTAACAGGAAT  
 GCCTGTGTCTGCTTTTACTGTTATTCTCTCCAAAGCTTACCCAGCAATAGGAACTCCCATACCATTTGATAAAATTT  
 TGTATAACAGGCAACAGCATTATGACCCAAGGACTGGAATCTTTACTTGTGATACAGGAATATACTATTTTTTCA  
 TACCACGTGCATGTGAAAGGACTCATGTTTGGGTAGGCCTGTATAAGAATGGCACCCCTGTAATGTACACCTATGA  
 TGAATACACCAAAGGCTACCTGGATCAGGCTTCAGGGAGTGCCATCATCGATCTCACAGAAAATGACCAGGTGTGGC  
 TCCAGCTTCCCAATGCCGAGTCAAATGGCCTATACTCCTCTGAGTATGTCCACTCCTCTTTCTCAGGATTCTAGTG  
 GCTCCAAT**GTA**CTACAAGGGCGAATTCGTTTAAACCTGCAGGACTAGTCCCTTTAGTGAGGGTTAATT

**FIGURE 39**

GTTGGTGACCAAGAGTACATCTCTTTTCAAATAGCTGGATTAGGTCCTCATGCTGCTGTGGTCATTGCTGGTCATCT  
TTGATGCAGTCACTGAACAGGCAGATTCGCTGACCCTTGTGGCGCCCTCTTCTGTCTTCGAAGGAGACAGCATCGTT  
CTGAAATGCCAGGGAGAACAGAACTGGAAAATTCAGAAGATGGCTTACCATAAGGATAACAAAGAGTTATCTGTTTT  
CAAAAAATTCTCAGATTTTCCTTATCCAAAGTCAGTTTTTAAGTGACAGTGGTAACTATTTCTGTAGTACCAAAGGAC  
AACTCTTTCTCTGGGATAAACTTCAAATATAGTAAAGATAAAAGTCCAAGAGCTCTTTCAACGTCTGTGCTGACT  
GCCAGCTCCTTCCAGCCCATCGAAGGGGGTCCAGTGAGCCTGAAATGTGAGACCCGGCTCTCTCCACAGAGGTTGGA  
TGTTCAACTCCAGTTCTGCTTCTTCAGAGAAAACAGGTCCTGGGGTCAGGCTGGAGCAGCTCTCCGGAGCTCCAGA  
TTTCTGCCGTGTGGAGTGAAGACACAGGCTCTTACTGGTGCAAGGCAGAAACGGTGACTCACAGGATCAGAAAACAG  
AGCCTCCAATCCCAGATTCACGTGCAGAGAATCCCCATCTCTAATGTAAGCTTGGAGATCCGGGCCCCGGGGGACA  
GGTGACTGAAGGACAAAACTGATCCTGCTCTGCTCAGTGGCTGGGGGTACAGGAAATGTCACATTCTCTGGGTACA  
GAGAGGCCACAGGAACCAGTATGGGAAAGAAAACCCAGCGTCCCTGTCAGCAGAGCTGGAGATCCCAGCTGTGAAA  
GAGAGTGATGCCGGCAAATATTACTGTAGAGCTGACAACGGCCATGTGCCTATCCAGAGCAAGGTGGTGAATATCCC  
TGTGAGAATTCCAGTGTCTCGCCCTGTCTCACCCCTCAGGTCTCCTGGGGCCAGGCTGCAGTGGGGGACCTGCTGG  
AGCTTCACTGTGAGGCCCTGAGAGGCTCTCCCCCAATCTTGTACCAATTTTATCATGAGGATGTCACCCTTGGAAC  
AGCTCGGCCCCCTCTGGAGGAGGGGCTCCTTCAACCTCTCTTTGACTGCAGAACATTCTGGAACTACTCCTGTGA  
GGCCAACAACGGCCTGGGGGCCAGTGCAGTGAGGCAGTGCCAGTCTCCATCTCAGGACCTGATGGCTATAGAAGAG  
ACCTCATGACAGCTGGAGTTCTCTGGGGACTGTTTGGTGTCTTGGTTTCACTGGTGTGCTTTGCTGTTGTATGCC  
TTGTTCCACAAGATATCAGGAGAAAGTTCTGCCACTAATGAACCCAGAGGGGCTTCCAGGCCAAATCCTCAAGAGTT  
CACCTATTCAAGCCCAACCCAGACATGGAGGAGCTGCAGCCAGTGTATGTCAATGTGGGCTCTGTAGATGTGGATG  
TGGTTTATTCTCAGGTCTGGAGCATGCAGCAGCCAGAAAGCTCAGCAAACATCAGGACACTTCTGGAGAACAAGGAC  
TCCCAAGTCATCTACTCTTCTGTGAAGAAATCTAACACTTGGAGGAATCAGAAGGGAAGATCAACAGCAAGGATGG  
GGCATCATTAAGACTTGCTATAAAACCTTATGAAAATGCTTGAGGCTTATCACCTGCCACAGCCAGAACGTGCCTCA  
GGAGGCACCTCCTGTCATTTTTGTCCTGATGATGTTTCTTCTCCAATATCTTCTTTTACCTATCAATATTATTGAA  
CTGCTGCTACATCCAGACACTGTGCAAATAAATTATTTCTGCTACCTTCAAAAAAAAAAAAAAAAAAAAAATGCAG



**FIGURE 40**

GGCACGAGGCTGCGCCAGGGCCTGAGCGGAGGCGGGGCGAGCCTCGCCAGCGGGGGCCCCGGGCCTGGCCATGCCTC  
ACTGAGCCAGCGCCTGCGCCTCTACCTCGCCGACAGCTGGAACCAAGTGCGACCTAGTGGCTCTCACCTGCTTCCTCC  
TGGGCGTGGGCTGCCGGCTGACCCCGGGTTGTACCACCTGGGCGCACTGTCCTCTGCATCGACTTCATGGTTTTTC  
ACGGTGCGGCTGCTTCACATCTTCACGGTCAACAAACAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAA  
GGACGTGTTCTTCTTCTTCTTCTTCTTCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGC  
CACGGGACAGTGACTTCCCAAGTATCCTGCGCCGCGTCTTCTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCC  
CAGGAGGACATGGACGTGGCCCTCATGGAGCACAGCAACTGCTCGTCGGAGCCCGGCTTCTGGGCACACCCTCCTGG  
GGCCAGGCGGGCACCTGCGTCTCCAGTATGCCAACTGGCTGGTGGTGCTGCTCCTCGTCATCTTCTGCTCGTGG  
CCAACATCCTGCTGGTCAACTTGCTCATTGCCATGTTTACGTTACACATTCGGCAAAGTACAGGGCAACAGCGATCTC  
TACTGGAAGGCGCAGCGTTACCGCCTCATCCGGGAATTCCACTCTCGGCCCGCGCTGGCCCCGCCCTTTATCGTCAT  
CTCCCACTTGCGCCTCCTGCTCAGGCAATTGTGCAGGCGACCCCGGAGCCCCAGCCGTCTCCCCGGCCCTCGAGC  
ATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAACTTTCTG  
CTGGCACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCAGAAAGGTGGACTTGGCACT  
GAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCCTGAAAGTGCTGGAGCGGGAGGTCCAGCAGTGTAGCCGCG  
TCCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTCTGCCTTGCTGCCCCAGGTGGGCCGCCACCCCTGACCTGCCT  
GGGTCCAAAGACTTGAGCCCTGCTGGCGGACTTCAAGGAGAAGCCCCACAGGGGATTTTGCTCCTAGAGTAAGGCTC  
ATCTGGGCCTCGGCCCCCGCACCTGGTGGCCTTGTCCTTGAGGTGAGCCCCATGTCCATCTGGGCCACTGTCAGGAC  
CACCTTTGGGAGTGTATCCTTACAAACCACAGCATGCCCGGCTCCTCCAGAACCAGTCCCAGCCTGGGAGGATCA  
AGGCCTGGATCCCGGGCCGTTATCCATCTGGAGGCTGCAGGGTCTTGGGGTAACAGGGACCACAGACCCCTCACCA  
CTCACAGATTCCTCACACTGGGGAAATAAAGCCATTTAGAGGAAAAAAAAAAAAAAAAAAAA

**FIGURE 41**

GAGAGAACAGCGTGAGCCTGTGTGCTTGTGTGCTGAGCCCTCATCCCCCTCTGGGGCCAGGCTTGGGTTTCACCTGC  
AGAATCGCTTGTGCTGGGCTGCCTGGGCTGTCCTCAGTGGCACCTGCATGAAGCCGTTCTGGCTGCCAGAGCTGGAC  
AGCCCCAGGAAAACCCACCTCTCTGCAGAGCTTGCCAGCTGTCCCCGGGAAGCCAAATGCCTCTCATGTAAGTCTT  
CTGCTCGACGGGTGTCTCCTAAACCCTCACTCTTCAGCCTCTGTTTGACCATGAAATGAAGTGACTGAGCTCTATT  
CTGTACCTGCCACTCTATTTCTGGGGTGACTTTTGTGAGCTGCCAGAATCTCCAAGCCAGGCTGGTTCTCTGCATC  
CTTTCAATGACCTGTTTTCTTCTGTAACCACAGGTTGCGTGGTGAGAGGAAGCCTCGCAGAATCCAGCAGAATCCTC  
ACAGAATCCAGCAGCAGCTCTGCTGGGGACATGGTCCATGGTGCAACCCACAGCAAAGCCCTGACCTGACCTCCTGA  
TGCTCAGGAGAAGCCATGGGCCCCCTCTGTCTGTGTTCTGTCTTCACAAAGCTCAGCCTGTGGTGCGCTCCTTCT  
GACCCCAGCAGGTGGAGAGGAAGCTAAGCGCCCACCTCCCAGGGCTCCTGGAGACCCACTCTCCTCTCCAGTCCCA  
CGGCATTGCCGCAGGGAGGCTCGCATACCGAGACTGAGGACCGGCTCTTCAAACACCTCTTCCGGGGCTACAACCGC  
TGGGCGCGCCCGGTGCCAACACTTCAGACGTGGTGATTGTGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT  
GGATGAGAAGAACCAAATGATGACCACCAACGTCTGGCTAAAACAGGAGTGAGCGACTACAACTGCGCTGGAACC  
CCGCTGATTTTGGCAACATCACATCTCTCAGGTCCCTTCTGAGATGATCTGGATCCCCGACATTGTTCTCTACAAC  
AATGCAGATGGGGAGTTTGCAGTGACCCACATGACCAAGGCCACCTCTTCTCCACGGGCACGTGCACTGGGTGCC  
CCCGCCATCTACAAGAGCTCCTGCAGCATCGACGTACCTTCTTCCCCTTCGACCAGCAGAAGTGAAGATGAAGT  
TTGGCTCCTGGACTTATGACAAGGCCAAGATCGACCTGGAGCAGATGGAGCAGACTGTGGACCTGAAGGACTACTGG  
GAGAGCGGCGAGTGGGCCATCGTCAATGCCACGGGCACCTACAACAGCAAGAAGTACGACTGCTGCGCCGAGATCTA  
CCCCGACGTACCTACGCCTTCGTCATCCGGCGGCTGCCGCTCTTCTACACCATCAACCTCATCATCCCCTGCCTGC  
TCATCTCCTGCCTCACTGTGCTGGTCTTCTACCTGCCCTCCGACTGCGGCGAGAAGATCACGCTGTGCATTTGCGTG  
CTGCTGTCACTACCGTCTTCTGCTGCTCATCACTGAGATCATCCCGTCCACCTCGCTGGTCATCCCGCTCATCGG  
CGAGTACCTGCTGTTACCATGATCTTCGTCACCCCTGTCCATCGTCATACCCGTCTTCGTGCTCAATGTGCACCACC  
GCTCCCCCAGCACCCACACCATGCCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCGGTGGCTTCTGATG  
AACCGGCCCCCACCACCCGTGGAGCTCTGCCACCCCTACGCCTGAAGCTCAGCCCCTCTTATCACTGGCTGGAGAG  
CAACGTGGATGCCGAGGAGAGGGAGGTGGTGGTGAGGAGGAGGACAGATGGGCATGTGCAGGTCAATGTGGCCCCCT  
CTGTGGGCACCCTCTGCAGCCACGGCCACCTGCACTCTGGGGCCTCAGGTCCCAAGGCTGAGGCTCTGCTGCAGGAG  
GGTGAGCTGCTGCTATACCCACATGCAGAAGGCACTGGAAGGTGTGCACTACATTGCCGACCACCTGCGGTCTGA  
GGATGCTGACTCTTCGGTGAAGGAGGACTGGAAGTATGTTGCCATGGTCATCGACAGGATCTTCCTCTGGCTGTTTA  
TCATCGTCTGCTTCTGGGGACCATCGGCCTCTTTCTGCCTCCGTTCCCTAGCTGGAATGATCTAGACTGCACCTCCCT  
CGAGCTGGCTCCCAGGGCAAAGGGGAGGGTTCTTGATGTGAAGGGCTTTGAACAATGTTTAGATTTGGAGATGAG  
CCCAAAGTGCCAGGGAGAACAGCCAGGTGAGGTGGGAGGTTGGAGAGCCAGGTGAGGTCTCTCTAAGTCAGGCTGGG  
GTTGAAGTTTGGAGTCTGTCCGAGTTTGCAGGGTCTGAGCTGTATGGTCCAGCAGGGGAGTAATAAGGGCTCTTCC  
GGAAGGGGAGGAAGCGGGAGGCAGGCCTGCACCTGATGTGGAGGTACAGGCAGATCTTCCCTACCGGGGAGGGATGG  
ATGGTTGGATACAGGTGGCTGGGCTATTCCATCCATCTGGAAGCACATTTGAGCCTCCAGGCTTCTCCTTGACGTCA  
TTCCTCTCCTTCTTGTGCTGCAAAATGGCTCTGCACCAGCCGGCCCCCAGGAGGTCTGGCAGAGCTGAGAGCCATGGC  
CTGCAGGGGCTCCATATGTCCCTACGCGTGCAGCAGGCAAACAAGA

**FIGURE 42**

CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAGAATTA**ATG**GAAAGCAGA  
AAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATAA  
GGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTG  
ACTGCCCTTCAGAACTTCAGCACACACAGGAACCTCTTCCACAGTGGCACTTGCCAATTAATAAGCTGCTATTATA  
GCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTAA  
TAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAG  
GTGTGATAGCAGCAATTGTCCAACCTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATG  
TTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAAT  
GAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTG  
AGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTG  
ACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTAGAGCAAGCTAGGAATTGTTTC  
CCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATA  
CACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCCTGATATTTAAAGCATACTATTCTGCCATGC  
TTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTACCAAAAATTAACAAACTGAGATATGTTCCCA  
GTTG**TAGA**ATTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTG  
TTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAA

**FIGURE 43**

GTGGCGCCCCGACGCCCCACCCGAGTGGCCATGGAGAAGCCTTCGGGGCAGCCGTGGTGACCGTGTGGGACAGC  
**GATG**CACAACACCACGGAGAAGCCCACCGATGCCTACGGAGAGCTGGACTTCACGGGGGCGCGCCGCAAGCACAGCA  
 ATTTCTCCGGCTCTCTGACCGAACGGATCCAGCTGCAGTTTATAGTCTGGTACACGCACATGGGGCTTCCGTGCC  
 CCGAACCTGGTGGTGTCACTGCTGGGGGGATCGGGGGGCCCCGTCTCCAGACCTGGCTGCAGGACCTGCTGCGTGC  
 TGGGCTGGTGC GGCTGCCAGAGCACAGGAGCCTGGATTGTCACTGGGGGTCTGCACACGGGCATCGGCCGGCATG  
 TTGGTGTGGCTGTACGGGACCATCAGATGGCCAGCACTGGGGGCACCAAGGTGGTGGCCATGGGTGTGGCCCCCTGG  
 GGTGTGGTCCGGAATAGAGACACCCTCATCAACCCCAAGGGCTCGTTCCCTGCGAGGTACCGGTGGCGCGGTGACCC  
 GGAGGACGGGGTCCAGTTTCCCTGGACTACAATACTCGGCCTTCTTCTGGTGGACGACGGCACACACGGCTGCC  
 TGGGGGGCGAGAACCCTTCCGCTTGGCGCTGGAGTCTACATCTCACAGCAGAAGACGGGCGTGGGAGGGACTGGA  
 ATTGACATCCCTGTCTCTCTCTGATTGATGGTGTAGAGAAGATGTTGACGCGAATAGAGAAGCCACCCAGGC  
 TCAGTCTCCATGTCTCTCTGGCTGGCTCAGGGGGAGCTGCGGACTGCCTGGCGGAGACCCCTGGGAAGACACTCTGG  
 CCCCAGGGAGTGGGGGAGCCAGGCAAGGCGAAGCCCGAGATCGAATCAGGCGTTTCTTTCCCAAAGGGGACCTTGAG  
 GTCCTGCAGGCCCAGGTGGAGAGGATTATGACCCGGAAGGAGCTCCTGACAGTCTATTCTTCTGAGGATGGGTCTGA  
 GGAATTCGAGACCATAGTTTGAAGGCCCTTGTGAAGGCCTGTGGGAGCTCGGAGGCCTCAGCCTACCTGGATGAGC  
 TGGCTTTGGCTGTGGCTTGAACCGCGTGGACATTGCCAGAGTGAACCTCTTTCGGGGGGACATCCAATGGCGGTCC  
 TTCCATCTCGAAGCTTCCCTCATGGACGCCCTGTGAATGACCGGCCTGAGTTCGTGCGCTTGCTCATTTCCACGG  
 CCTCAGCCTGGGCCACTTCTGACCCCGATGCGCCTGGCCCAACTCTACAGCGCGGCGCCCTCCAACCTCGCTCATCC  
 GCAACCTTTTGGACCAGGCGTCCCACAGCGCAGGCACCAAAGCCCCAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGG  
 CCCCCTGACGTGGGGCATGTGCTGAGGATGCTGCTGGGGAAGATGTGCGCGCGGAGGTACCCCTCCGGGGGCGCCTG  
 GGACCCTCACCCAGGCCAGGGCTTGGGGGAGAGCATGTATCTGCTCTCGGACAAGGCCACCTCGCCGCTCTCGCTGG  
 ATGCTGGCCTCGGGCAGGCCCCCTGGAGCGACCTGCTTCTTTGGGCACTGTTGCTGAACAGGGCACAGATGGCCATG  
 TACTTCTGGGAGATGGGTTCCAATGCAGTTTCTCAGCTCTTGGGGCTGTTTGCTGCTCCGGGTGATGGCACGCTT  
 GGAGCCTGACGCTGAGGAGGCAGCACGGAGGAAAGACCTGGCGTTCAAGTTTGAGGGGATGGGCGTTGACCTCTTTG  
 GCGAGTGTATCGCAGCAGTGAGGTGAGGGCTGCCCGCCTCCTCCTCGTCTGCTGCGCGCTCTGGGGGATGCCACT  
 TGCCTCCAGCTGGCCATGCAAGCTGACGCCCGTGCCCTTCTTTGCCAGGATGGGGTACAGTCTCTGCTGACACAGAA  
 GTGGTGGGGAGATATGGCCAGCACTACACCCATCTGGGCCCTGGTTCTCGCCTTCTTTTGCCCTCCACTCATCTACA  
 CCCGCCTCATCACCTTCAGGAAATCAGAAGAGGAGCCACACGGGAGGAGCTAGAGTTTGACATGGATAGTGTCATT  
 AATGGGGAAGGCCTGTGCGGACGGCGGACCCAGCCGAGAAGACGCCGCTGGGGGTCCCGCGCCAGTCGGGCCGTCC  
 GGGTTGCTGCGGGGGCGCGTGC GGGGGGCGCGGTGCCTACGCCGCTGCTTCCACTTCTGGGGCGCGCGGTGACCA  
 TCTTCATGGGCAACGTGGTCAGCTACCTGCTGTTCTTGCTGCTTTTCTCGCGGGTGTGCTCGTGGATTTCAGCCG  
 GCGCGCGCCGGCTCCCTGGAGCTGCTGCTCTATTTCTGGGCTTTCACGCTGCTGTGCGAGGAACTGCGCCAGGGCCT  
 GAGCGGAGGCGGGGACGCTCGCCAGCGGGGGCCCCGGGCTGGCCATGCCTCACTGAGCCAGCGCCTGCGCCTCT  
 ACCTCGCCGACAGCTGGAACCACTGCGACCTAGTGCTCTCACCTGCTTCTCCTCGTGGGCGTGGGCTGCCGGCTGACC  
 CCGGGTTTGTACCACCTGGGCCGCACTGTCTCTGCATCGACTTCATGGTTTTACGGTGCGGCTGCTTCACATCTT  
 CACGGTCAACAAACAGCTGGGGCCCCAAGATCGTCATCGTGAGCAAGATGATGAAGGACGTGTTCTTCTTCTCTCT  
 TCCTCGGCGTGTGGCTGGTAGCCTATGGCGTGGCCACGGAGGGGCTCCTGAGGCCACGGGACAGTGACTTCCCAAGT  
 ATCCTGCGCCGCTTCTTACCGTCCCTACCTGCAGATCTTCGGGCAGATTCCCCAGGAGGACATGGACGTGGCCCT  
 CATGGAGCACAGCAACTGCTCGTGGAGCCCCGGCTTCTGGGCACACCCTCCTGGGGCCCAGCGGGGACCTGCGTCT  
 CCCAGTATGCCAACTGGCTGGTGGTGTGCTCCTCGTCATCTTCTGCTCGTGGCCAACATCCTGCTGGTCAACTTG  
 CTCATTGCCATGTTCACTTACACATTTCGGCAAAGTACAGGGCAACAGCGATCTCTACTGGAAGGCGCAGCGTTACCG  
 CCTCATCCGGGAATTCACCTCTCGGCCCCGCGTGGCCCCGCGCTTTATCGTCATCTCCCACTTGCCTCTGCTCA  
 GGCAATTGTGACGGCGACCCCGGAGCCCCAGCCGCTCCTCCCCGGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAG  
 GAAGCCGAGCGGAAGCTGCTAACGTGGGAATCGGTGCATAAGGAGAAGTTTCTGCTGGCACGCGCTAGGGACAAGCG  
 GGAGAGCGACTCCGAGCGTCTGGAGCGCACGTCCAGAAGGTGGACTTGGCACTGAAACAGCTGGGACACATCCGCG  
 AGTACGAACAGCGCTGAAAGTGTGGAGCGGGAGGTCCAGCAGTGTAGCCGCGTCTGGGGTGGGTGACG**TAG**GCC  
 GTTAGCAGCTCTGCCATGTTGCCCTCAGGTGGGCCGCCACCCCTTGACCTGCATGGGTCCAAAGAGTGAGCCATGCT  
 GGGCGATTTTAAGGAGAAGCCCCACAGGGGATTTTGCTCTTAGAGTAAGGCTCATGTGGGCTCGGCCCCCGCACC  
 TGGTGGCCTTGCTTGGAGGTGAGCCCCATGTCCATCTGGGCCACTGTGAGGACCACCTTTGGGAGTGTATCCTTA  
 CAAACCACAGCATGCCCGGCTCTCCAGAACAGTCCAGCCTGGGAGGATCAAGCGCTGGATCCCGGGCCGTTAT  
 CCATCTGGAGGCTGCAGGGTCTTGGGGTAACAGGGACCACAGACCCCTCACCACTCACAGATTCTCTCACACTGGGG  
 AAATAAAGCCATTTAGAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 44A**

CGATAATTGAAAACCCAGATGTCCACAGGATTTTCGGGAATCAAGGGTCAACAGTAGAGTCCCTCTGTGATGATGTT  
 GTCTCTGTACTCACCCTCCTGTGTGAGAAGCTGCAAGCCGCCATAAATGACAGCCAGCAGCTGCAGCTTCTCTACCT  
 GGAGTGCATCCTGTCTGTGCTCAGCAGCTCCTCCTCCTCCATGCACAGGCGCTTCACGGACCTGATCTGGA  
 AAAACCTCTGCCCTGCTCTCATCGTGATCTTGGGGAATCCAATTCATGACAAAACCATCACCTCTGCTCACACCAGC  
 AGCACAGTACCAGCCTGGAGTCGACTCTGCGTCTCCGGGAGTGTCTGACCACGGCCGAGGATCAGGCTGCTCCTG  
 CACTGCGCCGCCCCTGAGCGGACCTGTGGCTCGGACTATCTATTACATCGCAGCCGAGCTGGTCCGGCTGGTGGGGT  
 CTGTGGACTCCATGAAGCCCGTGTCCAGTCCCTCTACCACCGAGTGTCTCTACCCCCACCCAGCACCGGGTG  
 GAAGCCATCAAAATAATGAAAGAGATACTTGGGAGCCCACAGCGTCTCTGTGACTTGGCAGGACCCAGCTCCACTGA  
 ATCAGAGTCCAGAAAAAGATCAATTTCAAAAAGAAAGTCTCATCTGGATCTCCTCAAACCTCATCATGGATGGCATGA  
 CCGAAGCATGCATCAAGGGTGGCATCGAAGCTTGTATGCAGCCGTGTCTGTGTCTGCACCTTGTCTGGGTGCCCTG  
 GATGAGCTCAGCCAGGGGAAGGGCTTGAGCGAAGGTCAAGTGCACCTGCTGCTTCTGCGCCTTGAGGAGCTGAAGGA  
 TGGGGCTGAGTGGAGCCGAGATTCCATGGAGATCAATGAGGCTGACTTCCGCTGGCAGCGGCGAGTGTCTCTCAG  
 AACACACGCGGTGGGAGTCAGGGAACGAGAGGAGCCTTGACATCAGCATCAGTGTACCACAGACACAGGCCAGACC  
 ACTCTCGAGGGAGAGTTGGGTGAGCTACACCCGAGGACCATTCGGGAAACCACAAGAACAGTCTCAAGTCGCCAGC  
 CATCCCAGAGGGTAAGGAGACGCTGAGCAAAGTATTGGAACAGAGGCGGTAGACCAGCCAGATGTCGTGCAGAGAA  
 GCCACACGGTCCCTTACCCTGACATAACTAATTCTGTCTCAGTAGACTGCAGGACAAGGTCCTATGGATCTAGGTAT  
 AGTGAGAGCAATTTTAGCGTTGATGACCAAGACCTTTCTAGACAGAGTTTGATTCTGTGATCACTACTCTATGGC  
 AGCAGAAAAGGACTCGGGCAGGTCCGACGTGTGACACATTGGGTGCGACAACCTGTTCACTAGCCGATGAAGAGCAGA  
 CACCCCGGGACTGCCTAGGCCACCGGTCCCTGCGAAGTGCAGCCCTGTCTCTAAAAGTGTGAAGAACAGGAGGCG  
 GATCAGCACAGCGCCAGGCTGTTCATACAGTCCCTGGAAGGCCTCCTCCCTCGGCTCCTGTCTCTCCAATGTAGA  
 GGAGGTGGACACCGCTCTGCAGAACTTGCCTCTACTTTCTGCTCAGGCATGATGCACTCTCCTGGCTTTGACGGGA  
 ATAGCAGCCTCAGCTTCCAGATGCTGATGAACGCAGACAGCCCTTACACAGCTGCACACTGCGCCCTGCTCCTCAAC  
 CTGAAGCTCTCCCACGGTGACTACTACAGGAAGCGGCCGACCCTGGCGCCAGGCGTGATGAAGGACTTCATGAAGCA  
 GGTGCAGACCAGCGGCGTGCTGATGGTCTTCTCTCAGGCCTGGATTGAGGAGCTCTACCATCAGGTGCTCGACAGGA  
 ACATGCTTGGAGAGGCTGGCTATTGGGGCAGCCCAGAAGATAACAGCCTTCCCCTCATCACAAATGCTGACCGATATT  
 GACGGCTTAGAGAGCAGTGCCATTGGTGGCCAGCTGATGGCCTCGGCTGCTACAGAGTCTCCTTTGCCCCAGAGCAG  
 GAGAATTGATGACTCCACAGTGGCAGGCGTGGCATTGTCTCGCTATATTTCTGGTGGGCTGCTGGAGAAGCTTGATCG  
 ATACTTTATCAACCCCACTGACTGGTCAATGGCGGGGAGCTCCAAAGGGCTGGCCTTCACTCTGGGAGCTGAAGGC  
 ATCAAAGAGCAGAACCAGAAGGAGCGGGACGCCATCTGCATGAGCCTCGACGGGCTGCGGAAAGCCGACGGCTGAG  
 CTGCGCTCTAGGCGTTGCTGCTAACTGCGCCTCAGCCCTTGCCAGATGGCAGCTGCCTCCTGTGTCCAAGAAGAAA  
 AAGAAGAGAGGGAGGCCCCAAGAACCCAGTGATGCCATCACACAAGTGAAGTAAAGTGGAGCAGAACTGGAGCAG  
 ATTGGGAAGGTGCAGGGGGTGTGGCTGCACACTGCCACGTCTTGTGCATGGAGGCCATCCTCAGCGTAGGCCCTGGA  
 GATGGGAAGCCACAACCCGGACTGCTGGCCACAGTGTTTCAGGGTGTGTGAATACGTGGGCACCTGGAGCACAAC  
 ACTTCAGCGATGGTGCCTCGCAGCCCCCTCTGACCATCAGCCAGCCCCAGAAGGCCACTGGAAGCGCTGGCCTCCTT  
 GGGGACCCCGAGTGTGAGGGCTCGCCCCCGAGCACAGCCCGAGCAGGGGCGCTCCCTGAGCACGGCCCCCTGTCTGT  
 CCAGCCCTGTCCATCCAGGACCTCGTCCGGGAAGGCAGCCGGGGTGGGCGCTCCGACTTCCGCGGCGGGAGCCTCA  
 TGAGCGGGAGCAGCGCGGCCAAGGTGGTGTCTACCCTCTCCACGCAAGCCGACAGGCTCTTTGAAGATGCTACGGAT  
 AAGTTGAACCTCATGGCCTTGGGAGGTTTTCTTTTACCAGCTGAAGAAAGCATCGCAGTCTCAGCTTTTCCATTCTGT  
 TACAGATACAGTTGATTACTCTCTGGCAATGCCAGGAGAAGTTAAATCCACTCAAGACCGAAAAAGCGCCCTCCACC  
 TGTTCGGCTGGGGAATGCCATGCTGAGGATTGTGCGGAGCAAAGCACGGCCCCCTGCTCCACGTGATGCGCTGCTGG  
 AGCCTTGTGGCCCCACACCTGGTGGAGGCTGCTTGCCATAAGGAAAGACATGTGTCTCAGAAGGCTGTTTCCTTCAT  
 CCATGACATACTGACAGAAGTCTCACTGACTGGAATGAGCCACCTCATTTTCACTTCAATGAAGCACTCTTCCGAC  
 CTTTCGAGCGCATTATGCAGCTGGAATTGTGTGATGAGGACGTCCAAGACCAGGTTGTACATCCATTGGTGAGCTG  
 GTTGAAGTGTGTTCCACGCAGATCCAGTCGGGATGGAGACCTTGTTCAGTGCCCTGGAAACAGTGCATGGCGGGAA  
 CAAGTCAGAGATGAAGGAGTACCTGGTGGTGTACTTCCATGGGAAAAGGCCAAGCTCCAGTGTGTTGATGTATTG  
 AAGCTTTTCTCAATACTGACAACATCCAGGTCTTTGCTAATGCAGCCACTAGCTACATCATGTGCCTTATGAAGTTT  
 GTCAAAGGACTGGGGGAGGTGGACTGTAAAGAGATTGGAGACTGTGCCCCAGCACCCGGAGCCCCGTCCACAGACCT  
 GTGCTCCCCGCCCTGGATTACCTCAGGCGCTGCTCTCAGTTATTGGCCAAAATCTACAAAATGCCCTTGAAGCCAA  
 TATTCCCTTAGTGGGAGACTTGCCGGCTTGCCCTCGAAGACTTCAGGAACAGTCAGCCAGCAGTGAGGATGGAATTGAA  
 TCAGTCTGTCTGATTTTGTGATGATGACACCGGTCTGATAGAAGTCTGGATAATCCTGCTGGAGCAGCTGACAGCGGC  
 TGTGTCCAATTGTCCACGGCAGCACCACCAACTCTGGATTTACTCTTTGAGCTGTTGAGAGATGTGACGAAAA  
 CACCAGGACCAGGGTTTGGTATCTATGCAGTGGTTCACTCCTCCTTCTGTGATGTCCGTTTGGCTCC

**FIGURE 44B**

GCCGGAGCCATAAAGACCATTCTACTGGGATATGGCCTCTGCCAATTTCAAGCACGCTATTGGTCTGTCTCTGTGAG  
 CTGGTGGTGGAGCACATTCAAAGCTTTCTACATTAGATATCAGGTACGAGAGCATGATCAATACCATGCTGAAGGA  
 CCTCTTTGAGTTGCTGGTCGCCTGTGTGGCCAAGCCCACTGAAACCATCTCCAGAGTGGGCTGCTCCTGTATTAGAT  
 ACGTCCTTGTGACAGCGGGCCCTGTGTTCACTGAGGAGATGTGGAGGCTTGCCCTGCTGTGCCCTGCAAGATGCGTTC  
 TCTGCCACACTCAAGCCAGTGAAGGACCTGCTGGGCTGCTTCCACAGCGGCACGGAGAGCTTCAGCGGGGAAGGCTG  
 CCAGGTGCGAGTGGCGGCCCCGTCCTCCTCCCCAAGTGCCGAGGCGGAGTACTGGCGCATCCGAGCCATGGCCCCAGC  
 AGGTGTTTATGCTGGACACCCAGTGCTCACCAGACACCAAAACAACCTTTGACCACGCTCAGTCCCTGCCAGCTCATT  
 ATTGAGCTGCCTCCTGATGAAAAACCAATGGACACACCAAGAAAAGCGTGTCTTTCAGGGAAATTGTGGTGAGCCT  
 GCTGTCTCATCAGGTGTTACTCCAGAACTTATATGACATCTTGTTAGAAGAGTTTGTCAAAGGCCCTCTCCTGGAG  
 AGGAAAAGACGATACAAGTGCCAGAAGCCAAGCTGGCTGGCTTCCCTCAGATACATCTCTATGCAGAACTTGGCAGTC  
 ATATTGACCTGCTGCTGGACTCTTATAGGACTGCCAGGGAGTTTGACACCAGCCCCGGGCTGAAGTGCTGCTGAA  
 GAAAGTGTCTGGCATCGGGGGCGCCGCCAACCTCTACCGCCAGTCTGCGATGAGCTTTAACATTTATTTCCACGCCC  
 TGGTGTGTGCTGTTCTACCAATCAAGAAACCATCACGGCCGAGCAAGTGAAGAAGGTCCTTTTTGAGGACGACGAG  
 AGAAGCACGGATTCTTCCCAGCAGTGTTTCATCTGAGGATGAAGACATCTTTGAGGAAACCGCCAGGTGAGCCCCC  
 GAGAGGCAAGGAGAAGAGACAGTGGCGGGCACGGATGCCCTTGCTCAGCGTCCAGCCTGTGAGCAACGAGATTGGG  
 TGTGGCTGGTCAAGAGGCTGCACAAGCTGTGCATGGAAGTGTGCAACAACTACATCCAGATGCACCTGGACCTGGAG  
 AACTGTATGGAGGAGCCTCCCATCTTCAAGGGCGACCCGTTCTTCATCCTGCCCTCCTTCCAGTCCGAGTCATCCAC  
 CCCATCCACCGGGGGCTTCTCTGGGAAAGAAACCCCTTCCGAGGATGACAGAAGCCAGTCCCGGGAGCACATGGGCG  
 AGTCCCTGAGCCTGAAGGCCGGTGGTGGGGACCTGCTGCTGCCCCCAGCCCCAAAGTGGAGAAGAGGATCCCAGC  
 CGGAAGAAGGAGTGGTGGGAGAATGCGGGGAACAAAATCTACACCATGGCAGCCGACAAGACCATTTCAAAGTTGAT  
 GACCGAATACAAAAAGAGGAAACAGCAGCACAACTGTCCGCGTTCCCAAGAGGTCAAAGTGGAGAAGAAAGAGGAG  
 AGCCACTGGGTCCCAGGGGCCAGGACTCCCCGCTGCTTCAGCGTCCCCAGCACTTGATGGACCAAGGGCAAAATGCGG  
 CATTCTTCAGCGCAGGCCCCGAGCTGCTGCGACAGGACAAGAGGCCCGCTCAGGCTCCACCGGGAGCTCCCTCAG  
 TGTCTCGGTGAGAGACGAGAAGCACAGATCCAGGCATGGACCAACATGGTGCTAACAGTTCTCAATCAGATTGAGA  
 TTCTCCCAGACCAGACCTTCACGGCCCTCCAGCCCCGAGTGTTCCCGTGTCATCAGTCAGCTGACCTGTACAGTGACC  
 GACATCAGAGTTGCGCAGGCTGTGAGGGAGTGGCTGGGCAGGGTGGGCCGTGTCTATGACATCATTTGTG**TAG**CCGAC  
 TCCTGTTCTACTCTCCCAACCAATAACAGTAGTGAGGGTTAGAGTCCCTGCCAATACAGCTGTTGCATTTTCCCCACC  
 ACTAGCCCCACTTAACTACTACTACTGTCTCAGAGAACAGTGTTTCCCTAATGTAAAAAGCCTTTCCAACCACTGAT  
 CAGCATTGGGGCCATACTAAGGTTTGTATCTAGATGACACAAACGATATTCTGATTTTGCACATTATTATAGAAGAA  
 TCTATAATCCTTGATATGTTTCTAACTCTTGAAGTATATTTCCCAGTGCTTTTGCTTACAGTGTTGTCCCCAAATGG  
 GTCATTTTCAAGGATTACTCATTTGAAAACACTATATTGATCCATTTGATCCATCATTTAAAAAATAAATAACAATTC  
 CTAAGGCAATATCTGCTGGTAAGTCAAGCTGATAAACACTCAGACATCTAGTACCAGGATTATTAATTGGAGGAAG  
 ATTTATGGTTATGGGTCTGGCTGGGAAGAAGACAACATAAATACATATTCTTGGGTGTCATAATCAAGAAAGAGGT  
 GACTTCTGTTGTAATAAATCCAGAACACTTCAAAATTATTCCTAAATCATTAAGATTTTCAGGTATTCACCAATTT  
 CCCCATGTAAGGTACTGTGTTGTACCTTTATTTCTGTATTTCTAAAAGAAGAAAGTTCTTTCTAGCAGGGTTTGAA  
 GTCTGTGGCTTATCAGCCTGTGACACAGAGTACCCAGTGAAAGTGGCTGGTACGTAGATTGTCAAGAGACATAAGAC  
 CGACCAGCCACCCTGGCTGTTCTTGTGGTGTTTGTGTTCCATCCCCAAGGCAAACAAGGAAAGGAAAGGAAGAA  
 AAGGTGCCCTTAGTCCTTTGTTGCACTTCCATTTCCATGCCCCACAATTGTCTGAACATAAGGTATAGCATTTGGTTT  
 TTAAGAAAACAAAACATTAAGACGCAACTCATTTTATATCAACACGCTTGGAGGAAAGGGACTCAGGGAAGGGAGCA  
 GGGAGTGTGGGTGGGGATGGATTATGATGAAATCATTTTCAATCTTAAATATAATACAACAATCTTGCAAAATTA  
 TGGTGTGAGTTACACAAGCTCTAGTCTCAAAATGAAAGTAATGGAGAAAGACACTGAAATTTAGAAAAATTTGTGCGA  
 TTTAAATATTTCTCCTATCTACCAAGTAAAGTTACCCTATGTTTGATGCTTTTGCAATTCAGACCAATATTTAGGT  
 GGATATTTCTAAGTATTACTAGAAAAATACGTTTGAAAGCTTTATCTTATTATTTACAGTATTTTATATTTCTTACA  
 TTATCCTAATGATTGAAAACCTCCTCAATCAAGCTTACTTACACACATTCTACAGAGTTATTTAAGGCATACATTATA  
 ATCTCCCAGCCCCATTTCATAATGAATAAGTCACCCTTTAAATATAAGACACAAATTCTACAGTATTGAAATAAGGAT  
 TTAAAGGGGTATTTGTAAACTTTGCCCTCCTTGAGAAATATGGAACCTACCTTAGAGGTTAAGAGGAAGGCAGTGTTT  
 TGACTTCTTTAGGTGATCTGAAAAAACACCCCTATCATCCAGTGTACCATCTAGAGATCACCACAGAATCCATTTT  
 TTTCCAGTTCACAAAACACTCTGTTTGCCCTTCAAGTTTACTCCTAGACAATAATTCAAGTTTGAAGAACAGGTA  
 ATCAGCTATTTGATCTTAAAGGCAATGAATTGTTGGGATATCAGTGAACCTATGTTGTATACTTTTGAATTTTACA  
 TTTTATAAATGGAATTGAAAGTTGGATAACTGCTTTTTTTTAAATTTTCCAACAGAAGTAACACCACAGTTGCTTT

**FIGURE 44C**

GTTCCTTTTATAGCTTACCTGAGGTCAGTTCTTCTTTGTGAACCTGTGAGTACTCCACAGTTTACTGGGGGAAAA  
GGCTTCAGTAAAGCAGAGGCTAGAATTACAGTATTTATACATAGCAACTTTTCATAAAGTAGAAAAATTCAAAGGAA  
GCTGTCTCAATTTGAGAATACCAGCTGGGCACGGTCG

FIGURE 45

CAGAGAGGCTGTATTTTCAGTGCAGCCTGCCAGACCTCTTCTGGAGGAAGACTGGACAAAGGGGGTACACATTCCTT  
CCATACGGTTGAGCCTCTACTGCGCTGGTGCTGGTACAGTTTCTTTCATGATGGTGGATCCCCAATGGCAATG  
AATCCAGTGCTACATACATTCATCCTAATAGGCCCTCCCTGGTTTAGAAGAGGCTCAGTTTCTGGTTGGCCCTCCCATTTG  
TGCTCCCTCTACCTTATTGCTGTGCTAGGTAACCTTGACAATCATCTACATTTGTGCGGACTGAGCACAGCCCTGCATGA  
GCCCATGTATATATTTCTTTGTCATGCTTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCAAAATGTCTGG  
CCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGTATGCTTGTCTGCTACAGATTTTGGCCATCCACTCCTTATCT  
GGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTTGACCGCTATGTGGCCATCTGTCACCCACTGCGCCATGCCAC  
AGTACTTACGTTGGCTCGTGTCAACAAAATTTGGTGTGGCTGCTGTGGTGC GG GGGGCTGCACTGATGGCACCCCTTC  
CTGCTTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACCAAGATGTCATG  
AAGCTGGCCTGTGATGATATCCGGGTCAATGTGCTTATGCGCTTATCGTCATCTCCGCCATTGGCCTGGACTC  
ACTTCTCATCTCCTTCTCATATCTGCTTATTCTTAAGACTGTGTTGGGCTTGACACAGTGAAGCCCAGGCCAAGGCAT  
TTGGCACTTGGCTCTCTCATGTGTGTGCTGTGTTTCATATTCTATGTACCTTTTCATTGGATTGTCCATGGTGCATCGC  
TTTAGCAAGCGGCGTGACTCTCGCTGCGCGTCATCTTGGCCAATATCTATCTGCTGGTTCCCTCCTGTGCTCAACCC  
AATTGTCTATGGAGTGAGACAAAGGAGATTTCGACAGCGCATCCTTCGACTTTTCCATGTGGCCACACACCGCTTCAG  
AGCCCTAGGGTGTGAGTCAAACTCTTTTCCATTCAGAGTCCCTTGATTAGATTATTAACATTTTGGAA  
GACAGTATTTCAGAAAAAAATTTCTTAATAAAAAATCAACTCAGATCCTTCAAATATGAACTGGTTGGGGAATC  
TCCATTTTTTCAATATTATTTTCTTCTTTGTTTTCTTGCTACATATAATTATTAATACCCTGACTAGGTTGTGGTTG  
GAGGTTATTACTTTTTCATTTTTACCATGCAGTCCAATCTAAACTGCTTCTACTGATGGTTTACAGCATTCTGAGAT  
AAGAATTGGTACATCTAGAGAACATTTTGCCAAAGGCCCTAAGCACGGCAAAAGGAAAAATAAACACAGAAATATAAAAAA  
GAGATAATCTAGCTTAAAACTATAAATCTCTTTCAGAACTCCCAACCACTTGGATCTCAGAAAAATGCTGCTTC  
AAAAAGACTTCTACAGAGAAAGAAATAATTTTTCTTGGACACTAGCACTTAAGGGGAAGATTGGAAGTAAAGCCTT  
GAAAAGAGTACATTTACCTACGTTAATGAAAGTTGACACACTGTTCTGAGAGTTTTTCACAGCATATGGACCCCTGTTT  
TTCCTATTTAATTTTTCTTATCAACCCTTTAATTAGGCAAGATATTATAGTACCCTCATTGTAGCCATGGGAAAAAT  
TGATGTTTCAGTGGGGATCAGTGAATTAATGGGGTCAACAAGTATAAAAAATTAAGAGAGTTTTCATGCCC  
ATATCATATGATGTGGAAGAACTGTTAGAGAGACCAACAGGTTAGTGGGTTAGAGATTCCAGAGTCTTACATTTT  
CTAGGAGGAGTATTTAATTTCTTCTCTACTATCCAGTGTGTTATTAGGAATTTCTGGCAACAGAACTCATGGCTT  
TAATCCCACTAGCTATTGCTTATTGTCTGGTCCAATTGCCAATTACCTGTGCTTGGGAAGAAGTGATTTCTAGGTT  
CACCATTATGGAAGATTCTTATTTCAGAAAGTCTGCATAGGGCTTATAGCAAGTTATTATTTTTTAAAGTTCATAG  
GTGATTCTGATAGGCAGTGAAGTTAGGGAGCCACAGTATGATGGGAAGTATGGAATTGGCAGGTTCTGAAGATAAC  
ATTGGCCTTTTGGTGTGACTCGTAGCTGGAAAGTGAAGGAACTCTCAGGACCATGCTTTATTTGGGGCTTTGTGCA  
GTATGGAACAGGGACTTTGAGACCAGGAAGCAATCTGACTTAGGCATGGGAATCAGGCATTTTTGCTCTGAGGGG  
CTATTACCAAGGGTTAATAGGTTTCATCTTCAACAGGATATGACAACAGTGTTAACCAAGAACTCAAATTACAAAT  
ACTAAAACATGTGATCATATATGTGGTAAAGTTTCATTTTCTTTTCAATCCTCAGGTTCCCTGATATGGATTCCATAT  
AACATGCTTTTCACTCCCTTTTGTAAATGGATATCATATTTTGAAATGGCTATTTAATACTTGTATTGTGCTGCTGGACT  
TGAAGCCCATGAGGCACTGTTTATTATTGAATGTATCTGTTTCATGTTGCTCTTTGCTCATCATGTAAT  
CCCCAGCAAAGTGCCTAGAACAATAATAGTGCTTATGCTTGACACCGGTTATTTTCTGCTCATCAAACCTGATTCTCTGT  
TCCTGAACACATAGCCAGGCAATTTTCCAGCCTTCTTTGAGTTGGGTATTATTAATTTCTGGCCATTACTTCCAATG  
TGAGTGGAAAGTGACATGTGCAATTTCTATACCTGCTCATAAAACCCCTCCCATGTGCAGCCTTTTCATGTTGACATTA  
AATGTGACTTGGGAAGCTATGTGTTACACAGAGTAATCACCAGAAGCTGGATTCTTGAAAAAAGCTGTCGAGAGCC  
AAACCTCTGTCTCATTTTGAACATCCCCTTGTATTGTTACGAGGCAAGTTGGATAAGTGAAAAATAAAGTACTATTGTGT  
CAAGAAAAA



**FIGURE 46**

AGCACCTTGGCACAGCTGAAGCAGAGGAACACGCTGAAGGATGGTATCATCATGATCCAGACGCTGCTGATCATCCT  
CTTCATCATCGTGCCTATCTTCCTGCTGCTGGACAAGGATGACAGCAAGGCTGGCATGGAGGAAGATCACACCTACG  
AGGGCCTGGACATTGACCAGACAGCCACCTATGAGGACATAGTGACGCTGCGGACAGGGGAAGTGAAGTGGTCTGTA  
GGTGAGCACCCAGGCCAGGAGTGAGAGCCAGGTCGCCCCATGACCTGGGTGCAGGCTCCCTGGCCTCAGTGAAGTGGTCTGTA  
TCGGAGCTGCCTGGCTCATGGCCCAACCCCTTTCCCGGACCCCCAGCTGGCCTCTGAAGCTGGCCCACCAGAGCTG  
CCATTTGTCTACCCCTGGTGTCCAGCTCTTGCCAAAGGGCCTGGAGTNNAAGGACAACAGGCANCACTTGGAGGGA  
GTTCTCTGGGGATGGACGGGACCCACCTT

**FIGURE 47**

CAGGAAGGTTCCCTCTCCAGTGGCCATGGGTAGCAACAGTGGGCAGGCTGGCCGCCACATCTATAAATCCCTAGCTG  
ATGATGGCCCCCTTTGACTCTGTGGAGCCGCCTAAAAGACCCACCAGCAGACTCATCATGCACAGCATGGCCATGTTT  
GGAAGAGAGTTCTGCTACGCGGTGGAGGCAGCGTATGTGACCCCAGTCCTGCTCAGCGTAGGTCTGCCCAGCAGCCT  
GTACAGCATTTGTGTGGTTCCCTCAGCCCCATCCTGGGATTCTTGCTGCAGCCCGTGGTTCGGATCGGCCAGCGACCACT  
GCCGGTCCAGGTGGGGCCGCCGGAGACCCTACATCCTCACCCTGGGAGTCATGATGCTCGTGGGCATGGCTCTGTAC  
CTCAATGGGGCTACTGTTGTAGCAGCTTTGATTGCTAACCCAAGGAGGAAGCTGGTTTGGGCCATAAGTGTACCAT  
GATAGGTGTCGTTCTCTTTGATTTTGCTGCCGACTTCATTGATGGGCCCATCAAAGCCTACTTATTTGATGTCTGCT  
CCCATCAGGACAAGGAGAAGGGCCTCCACTACCATGCCCTCTTCACAGGTTTTTGGAGGTGCCCTGGGTTACCTTTTG  
GGTGCTATAGACTGGGCCCATCTGGAGCTGGGAAGACTGTTGGGTACAGAAATCCAGGTCATGTTCTTCTCTCTGCT  
ATTGGTGCTCACTTTGTGTTTTACTGTTTCATCTGTGCAGTATCTCTGAAGCCCCACTTACAGAGGTTGCAAAGGGCA  
TTCCCCACAGCAAACCCCTCAGGACCCTCCATTGTCATCAGATGGAATGTACGAGTATGGTTCTATCGAGAAAGTT  
AAAAATGGTTACGTAAATCCAGAGCTGGCAATGCAGGGAGCAAAAAACAAAAATCATGCTGAACAGACTCGCAGGGC  
AATGACATTAAAGTCACTGCTGAGAGCACTGGTGAACATGCCTCCTCACTACCGCTACCTTTGCATCAGCCACCTCA  
TTGGATGGACGGCCTTCCTGTCCAACATGCTGTTCTTCACAGATTTTCATGGGCCAGATTGTGTACCGCGGGGATCCC  
TATAGTGCACACAACCTCCACAGAGTTTCTCATCTACGAAAGAGGAGTCGAGGTTGGATGTTGGGGCTTCTGCATCAA  
CTCCGTGTTTTCTCACTTTATTCTTACTTTTACAGAAAGTTTTGGTATCCTACATTGGATTAAAGGGTCTTTACTTCA  
CGGGATATTTGCTGTTTGGCCTGGGGACGGGATTTATTGGGCTCTTCCCGAATGTCTACTCCACCCTGGTCCTGTGC  
AGCCTGTTTGGTGTAATGTCCAGCACCTGTACACTGTGCCCTTTAACCTCATTACTGAGTACCACCGCGAGGAAGA  
AAAGGAGAGGCAGCAGGCCCCAGGAGGGGACCCAGACAACAGCGTGAGAGGGAAGGGCATGGACTGCGCCACCCTCA  
CATGCATGGTGCAGCTGGCTCAGATCCTGGTCGGAGGTGGCCTGGGCTTCTGGTCAACACAGCCGGGACCGTTGTC  
GTCGTGGTGATCACAGCGTCTGCGGTGGCACTGATAGGCTGTTGCTTTGTGCTCTCTTTGTTAGATATGTGGATTA  
GTCAATAAAGAGACAATGACCCTAAAAA

**FIGURE 48**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCATCTTCATCATTCATAT  
 GAGGAAATAAGTGGTAAATCCTTGGAATACAATGAGACTCATCAGAAACATTTACATATTTTGTAGTATTGTTAT  
 GACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAGAAAGGGAACATGATGACCAACTGCTCCAACATGTCTCTAAGAA  
 AGGTTCCCGCAGACTTGACCCAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTCA  
 GATTTTCATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGGATCTCAAAACCTT  
 TGAATTCAACAAGGAGTTAAGATATTTAGATTTTGTCTAATAACAGACTGAAGAGTGAACCTGGTATTTACTGGCAG  
 GTCTCAGGTATTTAGATCTTTCTTTTAAATGACTTTGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTACAC  
 CTGGAAATCCTAGGTTTGAGTGGGGCAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATAC  
 TGTCTTCTTAGGATTCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAACAAAACCTGCACA  
 TTGTTTTACCAATGGACACAAATTTCTGGGTCTTTTGCCTGATGGAATCAAGACTTCAAAAATATTAGAAATGACA  
 AATATAGATGGCAAAAGCCAATTTGTAAGTTATGAAATGCAACGAAATCTTAGTTTAGAAAAATGCTAAGACATCGGT  
 TCTATTGCTTAATAAAGTTGATTTACTCTGGGACGACCTTTTCCTTATCTTACAATTTGTTTGGCATAACATCAGTGG  
 AACACTTTTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTACTCAAATACT  
 GTAATGAGAACTATAAAATTTGGAGCATGTACATTTTCAGAGTGTTTTACATTC AACAGGATAAAATCTATTTGCTTTT  
 GACCAAAATGGACATAGAAAACCTGACAATATCAAATGCACAAATGCCACACATGCTTTTCCCGAATTATCCTACGA  
 AATTTCCAATATTTAAATTTTGCCAATAATATCTTAACAGACGAGTTGTTTAAAAGAAGTATCCAACCTGCCTCACTTG  
 AAAACTCTCATTTTGAATGGCAATAAACTGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACACCCCTTGGA  
 AACTTTGGATCTGAGTCAAAATCTATTACAACATAAAAAATGATGAAAATTGCTCATGGCCAGAAAACCTGTGGTCAATA  
 TGAATCTGTATACAATAAATTTGTCTGATTCTGTCTTCAGGTGCTTGCCCAAAAGTATTCAAATACCTTGACCTAAAT  
 AATAACCAATCCAACTGTACCTAAAGAGACTATTTCATCTGATGGCCTTACGAGAACTAAATATTGCATTTAATTT  
 TCTAACTGATCTCCCTGGATGCAGTCATTTTCAGTAGACTTTTCAGTTCTGAACATTGAAATGAACCTTCTCTCAGCC  
 CATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAAACCTCAAAATGCGGGAAGAAATCCATTCCGGTGTACCTGT  
 GAATTA AAAAATTTTCATTTCAGCTTGAACATATTCAGAGGTTCATGATGGTTGGATGGTCAGATTCATACACCTGTGA  
 ATACCCTTTAAACCTAAGGGGAAGTGGTTAAAAGACGTTTCATCTCCACGAATTATCTTGCAACACAGCTCTGTTGA  
 TTGTCACCATTTGTGGTTATTTATGCTAGTTCTGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGG  
 TATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAAACAACCCAAGAACAACCTCAAGAGAAA  
 TGTCCGATTCCACGCATTTATTTTCATACAGTGAACATGATTCTCTGTGGTGAAGAATGAATTGATCCCCAATCTAG  
 AGAAGGAAGATGGTTCTATCTTGATTTGCCTTTATGAAAGCTACTTTGACCCTGGCAAAAGCATTAGTGAAAATATT  
 GTAAGCTTCATTGAGAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCAACTTTGTCCAGAATGAGTGGTGCCATTA  
 TGAATTCTACTTTGCCCACCACAATCTCTCCATGAAAATTTCTGATCATATAATTCTTATCTTACTGGAACCCATTC  
 CATTCTATTGCATTTCCACAGGTATCATAACTGAAAGCTCTCCTGGAAAAAAAAGCATACTTGGAAATGGCCCAAG  
 GATAGGCGTAAATGTGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAAT  
 GTATGAACTGCAGACATTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTC  
 TATAAAAATCCACAGTCCTTGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTGATACAACTTTATGATG  
 GCAATTTGACAATATTTATTAAATAAAAAATGGTTATTCCTTCATATCAGTTTCTAGAAGGATTCTAAGAATGT  
 ATCCTATAGAAACACCTTCACAAGTTTATAAGGGCTTATGGAAAAAGGTGTTTCATCCCAGGATTGTTTATAATCATG  
 AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGTAATCCAGCACTATGGGAGGCCAAGGTGGGTGACCCACGAGGT  
 CAAGAGATGGAGACCATCCTGGCCAACATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGTGAT  
 GGTGCACGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAAATCGCTTGAACCCGGGAGGTGGCAGTTGCAG  
 TGAGCTGAGATCGAGCCACTGCACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAA  
 GAAAAAATGGAAACATCCTCATGGCCACAAAATAAGGTCTAATTCAATAAATTATAGTACATTAATGTAATATAA  
 TATTACATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGGAAAAACATATTAATATGTTATAAACT  
 ATTAGGTTGGTGCAAACTAATTGTGGTTTTTGCATTGAAATGGCATTGAAATAAAAGTGTAAAGAAATCTATACC  
 AGATGTAGTAACAGTGGTTTTGGGTCTGGGAGGTTGGATTACAGGGAGCATTTGATTTCTATGTTGTGATTTCTATA  
 ATGTTTGAATTGTTTAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

**FIGURE 49A**

GTCACCTGGATGGTGTAAAGGAAACAAGAGACAGGAACAGAGCCCCCATCTCACCTCTGGGCTACCATAACAGAAAA  
 GCAGAATTGGCAGGAACTGAAAATGACTAGGAAGAGGACATACTGGGTGCCCAACTCTTCTGGTGGCCTCGTGAATC  
 GTGGCATCGACATAGGCGATGACATGGTTTCAGGACTTATTTATAAAACCTATACTCTCCAAGATGGCCCCCTGGAGT  
 CAGCAAGAGAGAAATCCTGAGGCTCCAGGGAGGGCAGCTGTCCCACCGTGGGGGAAGTATGATGCTGCCTTGAGAAC  
 CATGATTCCCCTCCGTCCCAAGCCGAGGTTTCCTGCCCCCAGCCCCCTGGACAATGCTGGCCTGTCTCTCTACCTCA  
 CCGTGTCTATGGCTCACCCCGCTCATGATCCAAAGCTTACGGAGTCGCTTAGATGAGAACACCATCCCTCCACTGTCA  
 GTCCATGATGCCTCAGACAAAAATGTCCAAAGGCTTACCCGCCTTTGGGAAGAAGAAGTCTCAAGGCGAGGGATTGA  
 AAAAGCTTCAGTGCTTCTGGTGATGCTGAGGTTCCAGAGAACAAAGTTGATTTTCGATGCACCTCTGGGCATCTGCT  
 TCTGCATTGCCAGTGTACTCGGGCCAATATTGATTATACCAAAGATCCTGGAATATTCAGAAGAGCAGTTGGGGAAT  
 GTTGTCATGGAGTGGGACTCTGCTTTGCCCTTTTCTCTCCGAATGTGTGAAGTCTCTGAGTTTCTCCTCCAGTTG  
 GATCATCAACCAACGCACAGCCATCAGGTTCCGAGCAGCTGTTTCCCTTTGCTTTGAGAAAGCTCATCCAATTTA  
 AGTCTGTAATACACATCACCTCAGGAGAGGCCATCAGCTTCTTACCCTGGTATGTAAACTACCTGTTTGAAGGGGTG  
 TGCTATGGACCCCTAGTACTGATCACCTGCGCATCGCTGGTCATCTGCAGCATTTCTTCCCTACTTCATTATTGGATA  
 CACTGCATTTATTGCCATCTTATGCTATCCCCGGTTTTCCCACTGGAGGTATTTCATGACAAGATGGCTGTGAAGG  
 CTCAGCATCACACATCTGAGGTCAGCGACCAGCGCATCCGTGTGACCAGTGAAGTTCTCACTTGCATTAAGCTGATT  
 AAAATGTACACATGGGAGAAACCATTTGCAAAAATCATTTGAAGACCTAAGAAGGAAGGAAAGGAAAGCTATTGGAGAA  
 GTGCGGGCTTGTCCAGAGCCTGACAAGTATAACCTTGTTCATCATCCCCGAGTGGCCACAGCGGTCTGGGTTCTCA  
 TCCACACATCCTTAAAGCTGAAACTCACAGCGTCAATGGCCTTCAGCATGCTAGCCTCCTTGAATCTCCTTCGGCTG  
 TCACTGTTCTTTGTGCCTATTGCAGTCAAAGGCTCTACGAATTCGAAGTCTGCAGTGATGAGGTTCAAGAAGTTTTT  
 CCTCCAGGAGAGCCCTGTTTTCTATGTCCAGACATTACAAGACCCCAAGCTCTGGTCTTTGAGGAGGCCACCT  
 TGTATGGCAACAGACCTGTCCCGGGATCGTCAATGGGGCACTGGAGCTGGAGAGGAACGGGCATGCTTCTGAGGGG  
 ATGACCAGGCCTAGAGATGCCCTCGGGCCAGAGGAAGAAGGGAACAGCCTGGGCCAGAGTTGCACAAGATCAACCT  
 GGTGGTGTCCAAGGGGATGATGTTAGGGGTCTGCGGCAACACGGGGAGTGGTAAGAGCAGCCTGTTGTGAGCCATCC  
 TGGAGGAGATGCACTTGCTCGAGGGCTCGGTGGGGGTGTCAGGGAAGCCTGGCCTATGTCCCCAGCAGGCCTGGATC  
 GTCAGCGGGAACATCAGGGAGAACATCCTCATGGGAGGCGCATATGACAAGGCCCGATACCTCCAGGTGCTCCACTG  
 CTGCTCCCTGAATCGGGACCTGGAACCTTCTGCCCTTTGGAGACATGACAGAGATTGGAGAGCGGGGGCCCCAACCTCT  
 CTGGGGGGCAGAAACAGAGGATCAGCCTGGCCCGGCCGTCTATTCCGACCGTCAGATCTACCTGCTGGACGACCCC  
 CTGTCTGCTGTGGACGCCCACGTGGGGAAGCACATTTTTGAGGAGTGCATTAAGAAGACACTCAGGGGGAAGACGGT  
 CGTCCAGGTGACCCACCAGCTGCAGTACTTAGAATTTTGTGGCCAGGTCATTTTGTGGAAAATGGGAAAATCTGTG  
 AAAATGGAATCAGAGTGAGTTAATGCAGAAAAAGGGGAAATATGCCCAACTTATCCAGAGATGCACAAGGAAGCC  
 ACTTCGGACATGTTGCAGGACACAGCAAAGATAGCAGAGAAGCCAAAGGTAGAAAGTCAGGCTCTGGCCACCTCCCT  
 GGAAGAGTCTCTCAACGGAAATGCTGTGCCGGAGCATCAGCTCACACAGGAGGAGGATGGAAGAAGGCTCCTTGA  
 GTTGGAGGGTCTACCACCACTACATCCAGGCAGCTGGAGGTTACATGGTCTCTTGCATAATTTTCTTCTTTGTGGTG  
 CTGATCGTCTTCTTAACGATCTTCAGCTTCTGGTGGCTGAGCTACTGGTGGAGCAGGGCTCGGGGACCAATAGCAG  
 CCGAGAGAGCAATGGAACCATGGCAGACCTGGGCAACATTGCAGACAATCCTCAACTGTCTTCTACCAGCTGGTGT  
 ACGGGCTCAACGCCCTGCTCCTCATCTGTGTGGGGTCTGCTCCTCAGGGATTTTCACCAAGGTCACGAGGAAGGCA  
 TCCACGGCCCTGCACAACAAGCTCTTCAACAAGTTTTCCGCTGCCCCATGAGTTTCTTTGACACCATCCCAATAGG  
 CCGGCTTTTGAATGCTTCGACGGGACTTGGAAACAGCTGGACCAGCTCTTGCCCATCTTTTCAGAGCAGTTCTTGG  
 TCCTGTCTTAATGGTGATCGCCGTCTGTTGATTGTGAGTGTGCTCTCCATATATCTGTTAATGGGAGCCATA  
 ATCATGGTTATTTGCTTCAATTTATTATATGATGTCAAGGAGGCCATCGGTGTGTTCAAGAGACTGGAGAATATAG  
 CCGGTCTCCTTTATCTCCACATCCTCAATTCTCTGCAAGGCCTGAGCTCCATCCATGTCTATGGAAAACTGAAG  
 ACTTCATCAGCCAGTTTAAAGAGGCTGACTGATGCGCAGAATAACTACCTGCTGTTGTTTCTATCTTCCACACGATGG  
 ATGGCATTGAGGCTGGAGATCATGACCAACCTTGTGACCTTGCCGTTGCCCTGTTTCGTGGCTTTTGGCATTTCCTC  
 CACCCCTACTCCTTTAAAGTCATGGCTGTCAACATCGTGTGAGCTGGCGTCCAGCTTCCAGGCCACTGCCCGGA  
 TTGGCTTGGAGACAGAGGCACAGTTCACGGCTGTAGAGAGGATACTGCAGTACATGAAGATGTGTGTCTCGGAAGCT  
 CCTTTACACATGGAAGGCACAAGTTGTCCCGAGGGGTGGCCACAGCATGGGGAAATCATATTTCAAGATTATCACAT  
 GAAATACAGAGACAACACCCACCGTGCTTACGGCATCAACCTGACCATCCGCGGCCACGAAGTGGTGGGCATCG  
 TGGGAAGGACGGGCTTGGGAAGTCCTCCTTGGGCATGGCTCTCTCCGCTGGTGGAGCCATGGCAGGCCGGATT  
 CTCATTGACGGCTGGACATTTGCAGCATCGGCCTGGAGGACTTGGGGTCCAAGCTCTCAGTGATCCCTCAAGATCC  
 AGTGCTGCTCTCAGGAACCATCAGATTCAACCTAGATCCCTTTGACCGTCACACCGACCAGCAGATCTGGGATGCCT  
 TGGAGAGGACATTCTGACCAAGGCCATCTCAAAGTTCCCCAAAAGCTGCATACAGATGTGGTGGAAAACGGTGGGA  
 AACTTCTCTGTGGGGGAGAGGCAGCTGCTCTGCATTGCCAGGGCTGTGCTTCGCAACTCCAAGATCATC

**FIGURE 49B**

CTTATCGATGAAGCCACAGCCTCCATTGACATGGAGACAGACACCCTGATCCAGCGCACAAATCCGTGAAGCCTTCCA  
GGGCTGCACCGTGCTCGTCATTGCCACCGTGTCAACACTGTGCTGAACTGTGACCGCATCCTGGTTATGGGCAATG  
GGAAGGTGGTAGAATTTGATCGGCCGGAGGTACTGCGGAAGAAGCCTGGGTCATTGTTGCGAGCCCTCATGGCCACA  
GCCACTTCTTCACTGAGATTAAGGAGATGTGGAGACTTCATGGAGGCTGGCAGCTGAGCTCAGAGGTTACACAGCTG  
CAGCTTCGAGGCCCACAGTCTGCGACCTTCTTGTTGGAGATGAGAACTTCTCCTGGAAGCAGGGGTAAATGTAGGG  
GGGGTGGGATTGCTGGATGGAAACCCTGGAATAGGCTACTTGATGGCTCTCAAGACCTTAGAACCCAGAACCATC  
TAAGACATGGGATTCAGTGATCATGTGGTCTCC

**FIGURE 50**

GGTGTCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTGTGTCAGGAGGAGACAGCCTCCCGGCCCGGGGAGGA  
 CAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCCTGCCGTCAGCTGCCGGCCGAGTT  
 GGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGGAGATTG  
 TCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGATTTCAAAGC  
 TGGGCTCAGCCTCTGTTTCTTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATTCCAATC**ATG**TCTGTGAT  
 GGTGGTGAGAAAGAGGTGACACGGAATGGGAGAACTCCCAGGCAGGAACACCTTTTGCTGTGATGGCCGCGTCA  
 TGATGGCCCCGGCAAAAGGGCATTCTTCTACCTGACCTTTTCTCATCTGGGGACATGTACACTCTTCTTCGCTTT  
 GAGTGCCGCTACCTGGCTGTTTCAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCTTCTTTCTCCATGGC  
 TACACTGTTGAGGACCAGCTTCAGTGACCTGGAGTGATTCTCGGGCGCTACCAGATGAAGCAGCTTTCATAGAAA  
 TGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACACCGCCTCGTATCAAGAATTTCCAGATAAAC  
 AACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCCGGGCTCCCATTTGCAGCATCTG  
 TGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTACCGCTACT  
 TCTACCTCTTCTCCTTTCTCTCTCCCTCCTACAATCTATGTCTTCGCCTTCAACATCGTCTATGTGGCCCTCAAA  
 TCTTTGAAATTTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAACGTCTCTAGAAGTCCTCATTTGCTTCTTTAC  
 ACTCTGGTCCGTCGTGGGACTGACTGGATTTTCTACTTTCTCGTGGCTCTCAACCAGACAACCAATGAAGACATCA  
 AAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCCATGGCAATATTGTGAAGAACTGCTGTGAAGTG  
 CTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTATTTTGCCACTGGAGGAAAGTGGAAGTCGACCTCC  
 CAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCCCAGCCCCACAGAACACCTGAAGTCAAATGAGATGC  
 CGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAGAGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAG  
 AAG**TAG**CCTATCTATGGAAGAGACTTTTGTGTTGTTAATTAGGGCTATGAGAGATTTAGGTGAGAAGTTAAACC  
 TGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACTGTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATT  
 TTCTTGCTGCAAGCTTTTTTAAATTTCTGAAGTCAAGGCAGTGGCAGAAAGATGTCAGTCACCTCTGATAACTGGAAA  
 AATGGGTCTCTTGGGCCCTGGCACTGGTTCTCCATGGCCTCAGCCACAGGGTCCCCCTTGGAACCCCTCTCTTCCCTC  
 CAGATCCCAGCCCTCCTGCTTGGGGTCACTGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCC  
 CAAGCTGCTGCACGTGCTGAGTCCAGAGGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTTCTTGGGGT  
 CTTCAGGACTGAAGAGGAGGGAGAGTGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCACAAATCC  
 TTTTAGGAATGGGACAGGTACCTTCCACTTGTTGTAXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGTTTTTCTTTT  
 GACTCCTGCTCCCATTAGGAGCAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCAATTTCTTTTCTCAGAGGAAG  
 CCCGAGTGCTCACTTAAACACTATCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGA  
 AACCAAGGCACAGAGAGGCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACCAGT  
 TCTTCCATTAAAGCCTCGGCTGAGTGAGGGAAAGCCCAGCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCCTCGG  
 CCCACCTCTGGCTATGGTAACCACACTGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCC  
 CAGAGCCACTTCAACCTGGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAA  
 GATTTATGTATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGAT  
 GACTTATGCGGTGGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAAGGCGATTAACTGTGTCTAATGCA

FIGURE 51

**FIGURE 52**

CAGTCACCATGAAGCTGGGCTGTGTCCCTCATGGCCTGGGCCCTCTACCTTTCCTTGGTGTGCTCTGGGTGGCCAG  
ATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGTCTGCACTGAGGAGAGCAGCTGCCACACGGA  
GGATGACTTGACTGATGCAAGGGAAGCTGGCTTCCAGGTCAAGGCCACACTTTCAGTGAACCTTCCACCTGATTG  
TGTCCATGACTGGCTGATCCTCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAG  
GCCTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGCCTAACAG  
GGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCACTGCAGTGGCATCTTCCAGAGCCCTGGTC  
CTGGGATCCCAGAAACAGCATCTGTTGTGGCTATCACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTA  
CCCTCAGCTGAACCCCAAGCAGGAAGCCCCATGACCCTGAGTTGTCAGACAAAGTTGGCCCTGCAGAGGTGAGCTGC  
CCGCCTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAAATCCAGATCCCCA  
CAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTTGGAACAGAGCCCC  
CAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCTGCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGC  
TGCTCCAGGAAGTGTCTGAGGAGGCCCCCTGGGCCTCTGCCTCCGCCCAACCCCATCTTCTGAGGATCCAGGCT  
TTTCTTCTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATGCAGGATGTG  
AGAGTCCTCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAAAGGCTAC  
TGCTGAATAGAAGTAAACAGTTCATCCATGATCTCACTTAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCC  
TGTCTGCACATATGCATAAGTACTTTTACAAGTTGTCCCAGTGTTTTGTAGATAATGTAGTTAGGTGAGTGTAA  
ATAAATTTATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTC  
TAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATAC  
AGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTTTGGTCATTATACTT  
GGGGGGTTGGGGATGGTGGGATGTGTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTA  
TAATGCACAGGGCAGTACCCACAAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAACCCCA  
GCCTAATGAAACCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCTCATT  
CAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGTCTATGGTCTGTTCTTTAGTTCTAGTTTGTATCCCTCAA  
AGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAG  
TGCAGAGCCCTCATGATTAGGATTAGTGCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCATATG  
AGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCGACTCTGTCGTTGCCTTGA  
TCTTGAAGTTCAGCCTCCAGAACTATGAGAAATAAATCTGGTTGTTGTAGCCTAA



**FIGURE 53**

CCGGCTCGCGCCCTCCGGGCCCAGCCTCCCGAGCCTTCGGAGCGGGCGCCGTCCCAGCCCAGCTCCGGGGAAACGCG  
AGCCGCGATGCCTGGGGGGTGCTCCCGGGGCCCCGCCGCCGGGACGGGCGTCTGCGGCTGGCGCGACTAGCGCTGG  
TACTCCTGGGCTGGGTCTCCTCGTCTTCTCCACCTCCTCGGCATCCTCCTTCTCCTCCTCGGCGCCGTTCTGGCT  
TCCGCCGTGTCCGCCAGCCCCCGCTGCCGGACAGTGCCCCGCGCTGTGCGAGTGCTCCGAGGACGCGCGCACAGT  
CAAGTGCGTTAACCGCAATCTGACCGAGGTGCCACGGACCTGCCCGCCTACGTGCGCAACCTCTTCCTTACCGGCA  
ACCAGCTGGCCGTGCTCCCTGCCGGCGCCTTCGCCCCGCCGGCCGCGCTGGCGGAGCTGGCCGCGCTCAACCTCAGC  
GGCAGCCGCTGGACGAGGTGCGCGCGGGCGCCTTCGAGCATCTGCCAGCCTGCGCCAGCTCGACCTCAGCCACAA  
CCCACTGGCCGACCTCAGTCCCTTCGCTTTCTCGGGCAGCAATGCCAGCGTCTCGGCCCCCAGTCCCTTGTGGAAC  
TGATCCTGAACCACATCGTGCCCCCTGAAGATGAGCGGCAGAACCGGAGCTTCGAGGGCATGGTGGTGGCGGCCCTG  
CTGGCGGGCGTGCCTGCAGGGGCTCCGCCGCTTGGAGCTGGCCAGCAACCACTTCCTTTACCTGCCGCGGGATGT  
GCTGGCCCAACTGCCAGCCTCAGGCACCTGGACTTAAGTAATAATTCGCTGGTGAGCCTGACCTACGTGTCCTTCC  
GCAACCTGACACATCTAGAAAGCCTCCACCTGGAGGACAATGCCCTCAAGGTCCTTACAATGGCACCCCTGGCTGAG  
TTGCAAGGTCTACCCACATTAGGGTTTTCTGGACAACAATCCCTGGGTCTGCGACTGCCACATGGCAGACATGGT  
GACCTGGCTCAAGGAAACAGAGGTAGTGCAGGGCAAAGACCGGCTCACCTGTGCATATCCGGAATAATGAGGAATC  
GGGTCTCTTGGAAGTCAACAGTGCTGACCTGGACTGTGACCCGATTCTTCCCCCATCCCTGCAAACCTCTTATGTC  
TTCCTGGGTATTGTTTTAGCCCTGATAGGCGCTATTTCTCCTGGTTTTGTATTTGAACCGCAAGGGGATAAAAAA  
GTGGATGCATAACATCAGAGATGCCTGCAGGGATCACATGGAAGGGTATCATTACAGATATGAAATCAATGCGGACC  
CCAGATTAACAAACCTCAGTTCTAACTCGGATGTCTGAGAAATATTAGAGGACAGACCAAGGACAACCTCTGCATGAG  
ATGTAGACTTAAGCTTTATCCCTACTAGGCTTGCTCCACTTTTCATCCTCCACTATAGATAACAACGGACTTTGACTAA  
AAGCAGTGAAGGGGATTTGCTTCCTTGTTATGTAAAGTTTCTCGGTGTGTTCTGTTAATGTAAGACGATGAACAGTT  
GTGTATAGTGTTTTACCCTCTTCTTTTCTTGGAAGTCTCAACACGTATGGAGGGATTTTTCAGGTTTCAGCATGA  
ACATGGGCTTCTTGCTGTCTGTCTCTCTCAGTACAGTTCAAGGTGTAGCAAGTGTACCCACACAGATAGCATTCA  
ACAAAAGCTGCCTCAACTTTTTCGAGAAAAATACTTTATTATAAATATCAGTTTTATTCTCATGTACCTAAGTTGT  
GGAGAAAATAATTGCATCCTATAAACTGCCTGCAGACGTTAGCAGGCTCTTCAAAATAACTCCATGGTGCACAGGAG  
CACCTGCATCCAAGAGCATGCTTACATTTTACTGTTCTGCATATTACAAAAATAACTTGCAACTTCATAACTTCTT  
TGACAAAGTAAATTACTTTTTTGATTGCAGTTTATATGAAATGTACTGATTTTTTTTTTAATAAACTGCATCGAGAT  
CCAACCGACTGAATTGTTAAAAAATAAAGATTCTTAAAGAA

**FIGURE 54**

CGGCGAGCGAGCACCTTCGACGCGGTCCGGGGACCCCTCGTCGCTGTCCTCCCGACGCGGACCCGCGTGCCCCAGG  
CCTCGCGCTGCCCCGGCCGGCTCCTCGTGTCCCACTCCCGGCGCACGCCCTCCCGCGAGTCCCGGGCCCTCCCGCGC  
CCCTCTTCTCGGCGCGCGCGCAGC**ATG**GCGCCCCGCGAGGTCCTCGCGTTCGGGCTTCTGCTTGCCGCGGCGACGGC  
GACTTTTGCCGAGCTCAGGAAGAATGTGTCTGTGAAAACCTACAAGCTGGCCGTAAACTGCTTTGTGAATAATAATC  
GTCAATGCCAGTGTAATTAGTTGGTGCACAAAATACTGTCAATTTGCTCAAAGCTGGCTGCCAAATGTTTGGTGATG  
AAGGCAGAAATGAATGGCTCAAACTTGGGAGAAGAGCAAAACCTGAAGGGGCCCTCCAGAACAATGATGGGCTTTA  
TGATCCTGACTGCGATGAGAGCGGGCTCTTTAAGGCCAAGCAGTGCAACGGCACCTCCACGTGCTGGTGTGTGAACA  
CTGCTGGGGTCAAGAAGACAGACAAGGACACTGAAATAACCTGCTCTGAGCGAGTGAGAACCCTACTGGATCATCATT  
GAACTAAACACAAAGCAAGAGAAAAACCTTATGATAGTAAAAGTTTGGCGACTGCACTTCAGAAGGAGATCACAAAC  
GCGTTATCAACTGGATCCAAAATTTATCACGAGTATTTTGTATGAGAATAATGTTATCACTATTGATCTGGTTCAAA  
ATTCTTCTCAAAAAACTCAGAATGATGTGGACATAGCTGATGTGGCTTATTATTTGAAAAAGATGTTAAAGGTGAA  
TCCTTGTTTCATTCTAAGAAAATGGACCTGACAGTAAATGGGGAACAACCTGGATCTGGATCCTGGTCAAACTTTAAT  
TTATTATGTTGATGAAAAAGCACCTGAATTCTCAATGCAGGGTCTAAAAGCTGGTGTTATTGCTGTTATTGTGGTTG  
TGGTGATAGCAGTTGTTGCTGGAATTGTTGTGCTGGTTATTTCCAGAAAGAAGAGAATGGCAAAGTATGAGAAGGCT  
GAGATAAAGGAGATGGGTGAGATGCATAGGGAACCTCAATGCAT**TAA**CTATATAATTTGAAGATTATAGAAGAAGGGAA  
ATAGCAAATGGACACAAATTACAAATGTGTGTGCGTGGGACGAAGACATCTTTGAAGGTCATGAGTTTGTAGTTTA  
ACATCATATATTTGTAATAGTGAAACCTGTACTCAAAATATAAGCAGCTTGAAACTGGCTTTACCAATCTTGAAATT  
TGACCACAAGTGCTTATATATGCAGATCTAATGTAAAATCCAGAACTTGGAATCCATCGTTAAAATTATTTATGTG  
TAACATTCAAATGTGTGCATTAAATATGCTTCCACAGTAAATCTGAAAAACTGATTTGTGATTGAAAGCTGCCTTT  
CTATTTACTTGAGTCTTGACATACATACTTTTTTATGAGCTATGAAATAAACATTTTAACTG

**FIGURE 55A**

CAATTTCGGCCTCGCTCCTTGTGATTGCGCTAAACCTTCCGTCCTCAGCTGAGAACGCTCCACCACCTCCCCGGATCG  
 CTCATCTCTTGGCTGCCCTCCCCTGTTCTGATGTTATTTTACTCCCCGTATCCCCTACTCGTTCTTACAAATTCT  
 GTAGGTGAGTGGTTCAGCTGGTGCCTGGCCTGTGTCTCTTGGATGCCCTGTGGCTTCAGTCCGTCTCCTGTTGCCC  
 ACCACCTCGTCCCCTGGGCCGCTGATACCCAGCCCAACAGCTAAGGTGTGGATGGACAGTAGGGGGCTGGCTTCTC  
 TCACTGGTCAGGGGTCTTCTCCCCTGTCTGCCTCCCGGAGCTAGGACTGCAGAGGGGCCATCATGGTGTGCTGCAGG  
 CCCCCTGGCTGTCTCGCTGTGTGCTGCCCAGCCTCACACTGCTGGTGTCCCACCTCTCCAGCTCCCAGGATGTCTCCA  
 GTGAGCCCAGCAGTGAGCAGCAGCTGTGCGCCCTTAGCAAGCACCCACCGTGGCCTTTGAAGACCTGCAGCCGTGG  
 GTCTCTAACTTCACTTACCCTGGAGCCCGGATTTCTCCAGCTGGCTTTGGACCCCTCCGGGAACCAGCTCATCGT  
 GGGAGCCAGGAACCTCTTCACTCAGCTCAGCCTTGCCAATGTCTCTCTTCTTTCAGGCCACAGAGTGGGCCCTCCAGTG  
 AGGACACGCGCCGCTCCTGCCAAGCAAGGGAAGACTGAGGAGGAGTGTGAGAACTACGTGCGAGTCCCTGATCGTC  
 GCCGGCCGGAAGGTGTTTATGTGTGGAACCAATGCCTTTTCCCCCATGTGCACCAGCAGACAGGTGGGGAACCTCAG  
 CCGGACTATTGAGAAGATCAATGGTGTGGCCCGCTGCCCTATGACCCACGCCACAACCTCCACAGCTGTCATCTCCT  
 CCCAGGGGGAGCTCTATGCAGCCACGGTCATCGACTTCTCAGGTGCGGACCCTGCCATCTACCGCAGCCTGGGCAGT  
 GGGCCACCGCTTCGCACTGCCCAATATAACTCCAAGTGGCTTAATGAGCCAACTTCGTGGCAGCCTATGATATTGG  
 GCTGTTTGCATACTTCTTCTGCGGGAGAACGCTGAGGACGACTGTGGACGCACCGTGTACTCTCGCGTGGCCC  
 GCGTGTGCAAGAAATGACGTGGGGGGCGATTCTGTGTGGAGGACACATGGACCACATTATGAAGGCCCGGCTCAAC  
 TGCTCCCGCCCGGGCGAGGTCCCCTTCTACTATAACGAGCTGCAGAGTGCCCTTCCACTTGCCGGAGCAGGACCTCAT  
 CTATGGAGTTTTTCAACAACGTAACAGCATCGCGCTTCTGTGTCTGCGCCTTCAACCTCAGTGCTATCTCCC  
 AGGCTTTCAATGGCCCATTTTCGCTACCAGGAGAACCCAGGGCTGCCTGGCTCCCATAGCCAACCCCATCCCCAAT  
 TTCCAGTGTGGCACCTTGCCTGAGACCGGTCCCAACGAGAACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCCT  
 TTCCTGATGAGCGAGGCCGTGCAGCCGTGACACCCGAGCCCTGTGTACCCAGGACAGCGTGCCTTCTCACACC  
 TCGTGGTGGACCTGGTGCAGGCTAAAGACACGCTCTACCATGTACTCTACATTGGCACCCGAGTCGGGCACCATCCTG  
 AAGGCGCTGTCCACGGCGAGCCGACGCTCCACGGCTGCTACCTGGAGGAGCTGCACGTGCTGCCCCCGGGCGCCG  
 CGAGCCCTGCGCAGCCTGCGCATCCTGCACAGCGCCCGCGCGCTCTTCGTGGGGCTGAGAGACGCGCTCCTGCGGG  
 TCCCCTGGAGAGGTGCGCCGCTACCGCAGCCAGGGGGCATGCCTGGGGGGCCGGGACCCGTACTGTGGCTGGGAC  
 GGAAGCAGCAACGTTGCAGCACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCCAGAATCACCAGCCTGTCC  
 TGTGCGGAATGTGACACGGGATGGGGGCTTCGGCCCATGGTCAACATGGCAACCATGTGAGCACTTGGATGGGGACA  
 ACTCAGGCTCTTGCTGTGTGAGCTCGATCCTGTGATTCCCCTCGACCCCGCTGTGGGGGCTTGAATGCTGGGG  
 CCAGCCATCCACATCGCAACTGCTCCAGGAATGGGGCGTGGACCCCGTGTGTCATCGTGGGCGCTGTGCAGCAGCTC  
 CTGTGGCATCGCTTCCAGGTCCGCCAGCGAAGTTGCAGCAACCCGTCTCCCGCCACGGGGGCGCGATCTTCGTGG  
 GCAAGAGCCGGGAGGAACGGTTCTGTAATGAGAACACGCTTGCCCGGTGCCATCTTCTGGGCTTCTTGGGGCTCC  
 TGGAGCAAGTGACGACGCAACTGTGGAGGGGGCATGCACTGCGGGCTGCGGCGCTGCGAGAACGGCAACTCCTGCCT  
 GGGCTGCGGCGAGTTCAAGACGTGCAACCCCGAGGGCTGCCCGAAGTGCAGCGCAACACCCCTGACGCGCTGGC  
 TGCCCGTGAACGTGACGACGGGCGGGGACGGCAGGAGCAGCGGTTCCGCTTACCTGCCGCGCGCCCTTGCAGAC  
 CCGCACGGCTGCACTTCCGCGAGGAGAAGGACCGAGACGAGGACCTGTCCCGCGGACGGCTCCGGCTCCTGCGACAC  
 CGACGCCCTGGTGGAGGTCTCCTGCGCAGCGGGAGCACCTCCCCGCACACGGTGAGCGGGGGCTGGGCCGCTGGG  
 GCCCCTGGTCTGCTGCTCCCGGACTGCGAGCTGGGCTTCCGCGTCCGCAAGAGAACGTGCACTAACCCGGAGCCC  
 CGCAACGGGGGCTGCCCTGCGTGGGGCATGCTGCCGAGTACCAGGACTGCAACCCCGAGGCTTGCCCACTTCCGGG  
 TGCTTGGTCTGCTGGACCTCATGGTCTCCATGCTCAGCTTCCGTGTGGTGGGGGTCACTATCAACGCACCCGTTCT  
 GCACCAGCCCCGACCTCCCCAGGTGAGGACATCTGTCTCGGGCTGCACACGGAGGAGGCACTATGTGCCACACAG  
 GCCTGCCAGGCTGGTGCCTTGGTCTGAGTGGAGTAAGTGCAGTACGACGAGGAGCCAGAGCCGAAGCCGGCACTG  
 TGAGGAGCTCCTCCCAGGTTCCAGCGCTGTGCTGGAAACAGCAGCCAGAGCCGCCCTGCCCTACAGCGAGATTCT  
 CCGTATCCTGCCAGCCTCCAGCATGGAGGAGGCCACCGACTGTGCAAGTAAAAGAAACCGGACCTACCTCATGCTG  
 CGGTCTCCAGCCCTCCAGCACCCCACTCCAAAGTCTGGACTCTTTCCACATCCTGCTCCAGACAGCCAAGCTTTG  
 TTGGGGTCCCCACTGCTTTGAGATGGGTCAATCTCATCCACTGGTGGCCACGGGCATCTCCTGCTTCTTGGGCTC  
 TGGGCTCCTTGAACCTTAGCAGTGTACCTGTCTTGCCAGCACTGCCAGCGTCAGTCCCAGGAGTCCACACTGGTCCATC  
 CTGCCACCCCAACCATTTGCACTACAAGGGCGGAGGCACCCCGAAGAATGAAAAGTACACACCCATGGAATTCAAG  
 ACCCTGAACAAGAATAACTTATCCCTGATGACAGAGCCAACTTCTACCCATTGCAGCAGACCAATGTGTACACGAC  
 TACTTACTACCCAAAGCCCCCTGAACAAACACAGCTTCCGGCCCGAGGCTCACCTGGACAACGGTGTCTCCCAACA  
 GCTGATACCGCGCTCCTGGGGACTTGGGCTTCTTGCTTTCATAAGGCACAGAGCAGATGGAGATGGGACAGTGGAGC  
 CAGTTTGGTTTTCTCCCTCTGCACTAGGCCAAGAAGTGTGCTGCTTCCGTGTGGGGGGTCCCATCCGGCTTCAGAGA  
 GCTCTGGCTGGCATTGACCATGGGGGAAAGGGCTGGTTTCAGGCTGACATATGGCCGAGGTCCAGTTC

**FIGURE 55B**

AGCCCAGGTCTCTCATGGTTATCTTCCAACCCACTGTCACGCTGACACTATGCTGCCATGCCTGGGCTGTGGACCTA  
CTGGGCATTTGAGGAATTGGAGAATGGAGATGGCAAGAGGGCAGGCTTTTAAGTTTGGGTTGGAGACAACTTCCTGT  
GGCCCCACAAGCTGAGTCTGGCCTTCTCCAGCTGGCCCCAAAAAAGGCCTTTGCTACATCCTGATTATCTCTGAAA  
GTAATCAATCAAGTGGCTCCAGTAGCTCTGGATTTTCTGCCAGGGCTGGGCCATTGTGGTGCTGCCCCAGTATGACA  
TGGGACCAAGGCCAGCGCAGGTTATCCACCTCTGCCTGGAAGTCTATACTCTACCCAGGGCATCCCTCTGGTCAGAG  
GCAGTGAGTACTGGGAAGTGGAGGCTGACCTGTGCTTAGAAGTCCTTTAATCTGGGCTGGTACAGGCCTCAGCCTTG  
CCCTCAATGCACGAAAGGTGGCCCAGGAGAGAGGATCAATGCCATAGGAGGCAGAAGTCTGGCCTCTGTGCCTCTAT  
GGAGACTATCTTCCAGTTGCTGCTCAACAGAGTTGTTGGCTGAGACCTGCTTGGGAGTCTCTGCTGGCCCTTCATCT  
GTTTCAGGAACACACACACACACACTCACACACGCACACACAATCACAATTTGCTACAGCAACAAAAAAGACATTG  
GGCTGTGGCATTATTAATTAAAGATGATATCCAGTC

**FIGURE 56**

CGCAGAAAGAGGAGGCGCTTGCCTTCAGCTTGTGGGAAATCCCGAAGATGGCCAAAGACAACCTCAACTGTTGCTTGC  
 TTCCAGGGCCTGCTGATTTTTTGGAAATGTGATTATTGGTTGTTGCGGCATTGCCCTGACTGCGGAGTGCATCTTCTT  
 TGTATCTGACCAACACAGCCTCTACCCACTGCTTGAAGCCACCGACAACGATGACATCTATGGGGCTGCCTGGATCG  
 GCATATTTGTGGGCATCTGCCTCTTCTGCCTGTCTGTTCTAGGCATTGTAGGCATCATGAAGTCCAGCAGGAAAATT  
 CTTCTGGCGTATTTTCATTCTGATGTTTATAGTATATGCCTTTGAAGTGGCATCTTGTATCACAGCAGCAACACAACA  
 AGACTTTTTTCACACCCAACCTCTTCCTGAAGCAGATGCTAGAGAGGTACCAAAAACAACAGCCCTCCAAACAATGATG  
 ACCAGTGGAAAAACAATGGAGTCACCAAAACCTGGGACAGGCTCATGCTCCAGGACAATTGCTGTGGCGTAAATGGT  
 CCATCAGACTGGCAAAAATACACATCTGCCTTCCGGACTGAGAATAATGATGCTGACTATCCCTGGCCTCGTCAATG  
 CTGTGTTATGAACAATCTTAAAGAACCTCTCAACCTGGAGGCTTGTAAACTAGGCGTGCCTGGTTTTTATCACAATC  
 AGGGCTGCTATGAACTGATCTCTGGTCCAATGAACCGACACGCCTGGGGGGTTGCCTGGTTTGGATTGTCATTCTC  
 TGCTGGACTTTTTGGGTTCTCCTGGGTACCATGTTCTACTGGAGCAGAATTGAATATTAAGCATAAAGTGTGCCAC  
 CATACTCCTTCCCCGAGTGACTCTGGATTTGGTGTGGAACCAGCTCTCTCCTAATATTCCACGTTTGTGCCCCAC  
 ACTAACGTGTGTCTTACATTGCCAAGTCAGATGGTACGGACTTCCTTTAGGATCTCAGGCTTCTGCAGTTCTCAT  
 GACTCCTACTTTTTCATCCTAGTCTAGCATTCTGCAACATTTATATAGACTGTTGAAAGGAGAATTTGAAAAATGCAT  
 AATAACTACTTCCATCCCTGCTTATTTTTAATTTGGGAAAATAAATACATTGGAAGGAACCTGTGTTATCACAGTAA  
 CCCAGAGCTGTATTTGGCTAGCAATCTGCCTGTATCTCTCACTATTATCTAAAAGAAACCTTCCAATGCTTCTGTTG  
 ATCTCAGTATTGTCAGGGGAACAGAGAAGTTGGGAAAAGATTACTGAAATATACCTTTTGCATTTCTTTCTAGAGTA  
 GCTCCCATATATGGAGATGGGTGATTCTCTTGATGCCACCTTCAGATCCTTTTATTCTCCAGAATAATTCTTAACAG  
 TGGTTCAAATTTCTTTTCATACCTTGAAGTATGTGTTTAGTAGCCTCAATTCTCCATTAATTAAAAGTGTGGGCTGG  
 GCGTGGGGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTGAGGAGTTCAAG  
 ACCAGCCTGGCCAACATGGTGAAACCCGCTCTCTACAAAATACAAAAATTAGCCAGGCGTGATGGCAGGTGCCTGT  
 AATCCTAGCTACTTGGCAGGCTAACGCAGGAGAATCACTTGACCGGGAGACAGAGGTTGCAGTGAGCTGAGATCGTA  
 CCTATTGCACTCCATCCTGGATGAAAGAGCCAGACTCTGTCTCAAACAAAACAAAAAGCGTGGGGACTTCTGGGGA  
 CAGACAAGGTGCCTGTTATATATTTACTCAGTCTTTGCCCTGAATGGTCTCAGCTTGAGACCATTTCAAACCTGGAGA  
 GAAGCAAGCCAGCCAATAGAATGGGGTGATTTACAGGGATTCTGTTTACTGTCAAATATTTCTCATCTGCACTAT  
 GTTTCATTTGTGGTCCTGAAGGAAATTCCTTATAACTCAACATTTGTCTGGTCTTATAAGTAAAGACAGCTTTAAAA  
 TCTGTTCACTTTCAAA

**FIGURE 57**

CCCGGCCCCGGGCTCGAGAATCAAGGGCCTCGGCCGCCGTCCCGCAGCTCAGTCCATCGCCCTTGCCGGGCAGCCCCG  
GCAGAGACCATGTTTGACAAGACGCGGCTGCCGTACGTGGCCCTCGATGTGCTCTGCGTGTTGCTGGCTGGATTGCC  
TTTTGCAATTTTTACTTCAAGGCATATTACTTCAAGGCATACCCCTTCCAACGAGGAGTATTCTGTAATGATGAGT  
CCATCAAGTACCCTTACAAAGAAGACACCATACCTTATGCGTTATTAGGTGGAATAATCATTCCATTCAGTATTATC  
GTTATTATTCTTGGAGAAACCCTGTCTGTTTACTGTAACCTTTTGCCTCAAATTCCTTTATCAGGAATAACTACAT  
AGCCACTATTTACAAAGCCATTGGAACCTTTTTATTTGGTGCAGCTGCTAGTCAGTCCCTGACTGACATTGCCAAGT  
ATTCAATAGGCAGACTGCGGCCTCACTTCTTGGATGTTTGTGATCCAGATTGGTCAAAAATCAACTGCAGCGATGGT  
TACATTGAATACTACATATGTCGAGGGAATGCAGAAAGAGTTAAGGAAGGCAGGTTGTCCTTCTATTCAGGCCACTC  
TTCGTTTTCCATGTACTGCATGCTGTTTGTGGCACTTTATCTTCAAGCCAGGATGAAGGGAGACTGGGCAAGACTCT  
TACGCCCCACACTGCAATTTGGTCTTGTGGCGTATCCATTTATGTGGGCCTTCTCGAGTTTCTGATTATAAACAC  
CACTGGAGCGATGTGTTGACTGGACTCATTCAGGGAGCTCTGGTTGCAATATTAGTTGCTGTATATGTATCGGATTT  
CTTCAAAGAAAGAACTTCTTTTAAAGAAAGAAAAGAGGAGGACTCTCATACAACTCTGCATGAAACACCAACAAGT  
GGAATCACTATCCGAGCAATCACCAGCCTTGAAAGGCAGCAGGGTGCCAGGTGAAGCTGGCCTGTTTTCTAAAGGA  
AAATGATTGCCACAAGGCAAGAGGATGCATCTTCTTCCTGG

**FIGURE 58**

**FIGURE 59**

GGAGCCGCGCCGCATCTCAGGCGCAGTCTCTAGGGGCTGTGCGCATCCTAGGGGGGGACATGTGCATCTCAGGGGGG  
 CTGCTCGCATCTGGGGGGTGTGTGTGCATCTCGGGGGGGCTGTTGCATCTACGCGGGGTGGCTGTGTCCGCATCTG  
 GAGGGGGCTGTGCGCAACCCGGGGGGGGTGTGCGCGCATCTAGCAGGGGCGGCTGTGCGCATTTCCGGGGGGGGCT  
 GTGCATATCTGGGGGGACACGTGCTTATCTCTGGGGGCGGCTGTGCGCATCTTGAGGGGTGTGTACATCTCGGGGGG  
 CCTGTGCATCTTGGGGGGCTGTGTGCATCCGCGGGGGCTGTGCGCATCTCGGGGTGCTGTGCGCTGCTCCTCTGAGC  
 TCTGCTCTTTCTTGACGCGTTTGCTCAGCC**ATG**GAGGGCGGGGCCGCGGCAGCCACCCACAGCACTGCCCTACT  
 ACGTGGCCTTCTCCAGCTGCTGGGCCTGACCTTGGTGGCCATGACCGGCGCGTGGCTCGGGCTGTACCGAGGCGGC  
 ATTGCCTGGGAGAGCGACCTGCAGTTCAACGCGCACCCCTCTGCATGGTCATAGGCCTGATCTTCTGCAGGGAAA  
 TGCCCTGCTGGTTTACCGTGTCTTCAGGAACGAAGCTAAACGCACCACCAAGGTCCTGCACGGGCTGCTGCACATCT  
 TTGCGCTCGTCATCGCCCTGGTTGGCTTGGTGGCGGTGTTGACTACCACAGGAAGAAGGGCTACGCTGACCTGTAC  
 AGCCTACACAGCTGGTGCGGGATCCTTGTCTTTGTCTGTACTTTGTGTCAGTGGCTGGTGGGCTTCAGCTTCTTCT  
 GTTCCCCGGAGCTTCATTCTCCTGCGGAGCCGCTACCGCCACAGCACATCTTCTTTGGTGTACCATCTTCTCTCC  
 TTCCCGTGGGCACCGCCCTGCTGGGCCTGAAGGAGGCACTGCTGTTCAACCTCGGGGGCAAGTATAGCGCATTTGAG  
 CCGGAGGTGTCTGGCCAACGTGCTGGGCCTGCTGCTGGCCTGCTTCGGTGGGCGGGTGTCTACATCTTGACCCG  
 GGCCGACTGGAAGCGGCCTTCCAGGCGGAAGAGCAGGCCCTCTCCATGGACTTCAAGACGCTGAGGCAGGGAGATA  
 GCGCGGCTCCAG**TGAT**GGCGCCCGGCCCTTGGGGGTTCGCGGGGTGTCTTCTTGCCTGCCCTGCTGAGGCGT  
 CTTACAGGACTGCAGGCTCCGAGAGTGGCTCTGGCAGCAGGCGGGCGCTGGGTGCAGGGGGATCCGTTTGATGCGT  
 CGTTTCTGGGGCAGGTCTCCGCTCCTCTGCTTCTCGTTTCTCCGCTGCTATAGACCAGTTCATTGTGTGTGGCTCC  
 CGTGTCTCTGTTGCCCCCTTCAGTGCAGAAGGCTTTGGGTAGACTTCGGGTGTTCCGGTCTGGTGCAGAGCACAGA  
 TCTTTAAAGAAGCGTTAGAGAGGTAGGTTCTACCCCTCTTGGTAGTAGATGCCTGGGGCAAGGCCAGGGGAACTGG  
 GGGGGCCTCAGGGACAGGCCTGGAAGGCCACGATGGCCTGCTGAATTCAAACAAGGAGTCCCTCCAGCCTGAATAA  
 CACGTGGCACAAATGGGCCCCGGCCTTTGGCAGAGGAGCAAGTGATATGATGTGTAAAGTATGTTGGTGGTGAAGCA  
 AGGTTCCCCAGGAGAGGGGAGGGACTGGCCCCCTGGGAAGCTGTGAGATGAGGCTGTGGCCCAGCTGTAGTCTGACC  
 TTAATCTTTCTTTAAACCCCTTTAGCCCTAGGATGGCTTTGGTGGGAGAGGGGATAGAAGCCCATGACTTCAGACAGA  
 CTTTCTCTTGGCAGATGCAGGCAGGCCTCCTCCAGGCTGCTCCAGACATGGGGGTTGGGGATGGGGGTACCTTGC  
 AGCCCCCTTCTGCTGGGGCTCCCTCCTTGTAGCACCCCTTGCGGCTCAGCTCTGGTTTCTCTCCAGGCTCACCC  
 AGGCTCTGCTCAGGCTGGGAGGCAGAGGGCACAAACCTTATAATTTTTTAAATGAAAAACCGCTGCTGCTGGCTGTG  
 GCTAGAGCCCCCTGGGGCTGCTGGAGCTGCTGCCTCTGTTCTGGAGGACGAGCCTTCTCCTTATCTGCTGCCATCT  
 TTCCAGGAAGTCAGGATGGAGTCAGACAATAACGATCATCCCCGTGGGTGTCTGCACATCACTCCAGCCCCATAA  
 AGAGTGTGATGTAGCTGAGTCACCATTTGGCTTCGGCCTGGAATAGTGTGTTAGAACACTGATCGTGTGCGAGGC  
 CAGGAGATCAAGACCATCCTGACTAACAAACACAGTGAAACCCCGTCTCTACTAAAAATACAAAAAATAGCCAGG  
 CGTGGTGGTGGGCGCTGTAGTCCCAGCTACTTGGGAGACAGGTCTCTACGGAATTCCTGTATTAGTCTATATGGT  
 TCTCCAAGAACTGAATGAATCCATTGGAGAAGCGGTGGATAACTAGCCACGACAAAATTTGAGAATACATAAAACAA  
 CGCATTCGCGAGGAAACATACAGAGGATGCCTTTTCTGTGATTGGGTGGGATTTTTTCCCTTTTTATGTGGATATAG  
 TAGTTACTTGTGACAAGAATAATTTTGAATAATTTCTATTAATATCAACTCTGAAGCTAATTGTACATAATCTCGA  
 GATTGTGTTTGTTCATAATAAAGTGAAGTGAATGTG



**FIGURE 60**

CGCCACCGCTGGGTGCGGCGAGGCCGGCGCG**ATG**CGGCAGCTGTGCCGGGGCCGCGTGCTGGGCATCTCGGTGGCCA  
TCGCGCACGGGGTCTTCTCGGGCTCCCTCAACATCTTGCTCAAGTTCCTCATCAGCCGCTACCAGTTCCTTCCTG  
ACCCTGGTGCAGTGCCTGACCAGCTCCACCGCGGCGCTGAGCCTGGAGCTGCTGCGGCGCCTCGGGCTCATCGCCGT  
GCCCCCTTCGGTCTGAGCCTGGCGCGCTCCTTCGCGGGGGTTCGCGGTGCTCTCCACGCTGCAGTCCAGCCTCACGC  
TCTGGTCCCTGCGCGGCCTCAGCCTGCCCATGTACGTGGTCTTCAAGCGCTGCCTGCCCTGGTCACCATGCTCATC  
GGCGTCTGGTGCTCAAGAACGGCGCGCCCTCGCCAGGGGTGCTGGCGGCGGTGCTCATCACCACCTGCGGCGCCGC  
CCTGGCAGGAGCCGGCGACCTGACGGGCGACCCCATCGGGTACGTACGGGAGTGCTGGCGGTGCTGGTGACGCTG  
CCTACCTGGTGCTCATCCAGAAGGCCAGCGCAGACACCGAGCACGGGCCGCTCACCGCGCAGTACGTATCGCCGTC  
TCTGCCACCCCGCTGCTGGTTCATCTGCTCCTTCGCCAGCACCGACTCCATCCACGCTGGACCTTCCCGGGCTGGAA  
GGACCCGGCCATGGTCTGCATCTTCGTGGCCTGCATCCTGATCGGCTGCGCCATGAACTTACCACGCTGCACTGCA  
CCTACATCAATTGCGCCGTGACCACCTCTCTGTTTATTGCCGGCGTGGTGGTGAACACCCTGGGCTCTATCATTTAC  
TGTGTGGCCAAGTTTCATGGAGACCAGAAAGCAAAGCAACTACGAGGACCTGGAGGCCAGCCTCGGGGAGAGGAGGC  
GCAGCTAAGTGGAGACCAGCTGCCGTTTCGTGATGGAGGAGCTGCCCGGGGAGGGAGGAAATGGCCGGTCAGAAGGTG  
GGGAGGCAGCAGGTGGCCCCGCTCAGGAGAGCAGGCAAGAGGTGAGGGGAGCCCCGAGGAGTCCCGCTGGTGGCT  
GGGAGCTCTGAAGAAGGGAGCAGGAGGTCGTTAAAGATGCTTACCTCGAGGTATGGAGGTTGGTTAGGGGAACCAG  
GTATATGAAGAAGGATTATTTGATAGAAAACGAGGAGTTACCCAGTCTT**TCGA**GAAGGAGGTGCATGTACGTACCTAT  
GTGCATACACTTATTTTATATGTTAGAAATGACGTGTTTTAATGAGAGGCCTCCCCGTTTTATTCTTTGAGGAGTGG  
GGAAGGGAAGAAAAGAAAGAAGCTGAAAGGTACTGACACAGAGCAACAAAATTAGCACCTGTGTGAATTATTTAGTG  
TGACTTCACCTGAGGCATCACAGAGACAAAAGAATGTGAAGCTACTTAACAAAAGTAAGGCAACGTTTCTGCTTCAGA  
CTCCTGGCACATTTACTTTTTGTCAATTATAACCATAACTAAATATCTGCATGTACCAAGAGTCCCTAAGCCACCCCC  
TCCAAAGATGGAGTGTAGAAATGATGACAGCACTTAGTAAGTTCAAAGATGACATTACGGGATGCATTTTTTGATGA  
TAGAACTACAGTTTTTATCGCCAGCTGGGCAAAGAGTATATTGCTGAAATGATATATAAATATATTGAATTGATGTT  
TACTGTTTATAGTCATCTGAAATATCATATTTACTCTGATTCTACTCACTTGTTTTTTAAAAATAAGTGTCTACTA  
TTGTATTATATATTGATAGAACTGTTAAAGCTATTTTGAAAATATGAGTTCTTAGCTTTAATCATGAAGTCTGAAG  
TTTGCTTTCAGTAATTATTTTAAAGTTGTTTTGGTTCATTGCTTTATAATATTTATTATTGAATGCCAAACCTGTT  
CTTTTTTTTACTGTGTCCAATATTCTTTCAAGCAAATGCAATGGCTGGAATATAATTCAGAATTAAGTGAACCCAG  
CCAGAAGAGGGACCACCTGTAAAGCAAGTCCTTTCAAGTTTCACTGCACATCCCAAACCATGTTACAAAAAGAGCAA  
CTGCTATATTCACATTATGATATTTTTCTATCTTAAATTTGTCAAAATAAAGTATGAGTCTAACTATTAAAAAAA  
AAAAAAA

**FIGURE 61**

ATTTCTCCAGGAGAACTCCACACTTGCACAATATCTTCTCCAAGGACAGAAGAGGGACAATATTTGTCCTTCCTACT  
GGATTTTGAAACCCTTTGCACTGAGTGTAGACTGTAGTTCTGTGACATACCATGAAGAGTGTGTGTGTGTTTAAAGG  
GAGCTACTGTCTTACCCAAAACCTGTGAATATAAAGTGTTTTTTCATGAATTGCTCATTATTCAGCCAGTCGTTAAT  
GAATTCATTCAACAAGTGTCTCTGAGATGCTAGACACTGGGGATTAAAAGAGGAACAACAGAGACAAGATCTCTGCC  
CTCCAGAACTGACAGTCTATTGAATGAGACAGTTGTCTAACAATCACAATCAAGTGTGATCAATCTCTGGTGACAG  
GACTCTAACCTAGAGGCATGTGCCTAATCTGGGGTGA

**FIGURE 62**

CAGGGGACAGGCTGCAGCCGGTGCA GTTACACGTTTTCTCCAAGGAGCCTCGGACGTTGTCACGGGTTTGGGGTCG  
GGGACAGAGCAGTGACCATGGCCAGGCTGGCGTTGTCTCCTGTGCCCAGCCACTGGATGGTGGCGTTGCTGCTGCTG  
CTCTCAGCTGAGCCAGTACCAGCAGCCAGATCGGAGGACCGGTACCGGAATCCCAAAGGTAGTGCTTGTTTCGCGGAT  
CTGGCAGAGCCACGTTTTCATAGCCAGGAAACGGGGCTTCACGGTGAAAATGCACTGCTACATGAACAGCGCCTCCG  
GCAATGTGAGCTGGCTCTGGAAGCAGGAGATGGACGAGAATCCCCAGCAGCTGAAGCTGGAAAAGGGCCGCATGGAA  
GAGTCCCAGAACGAATCTCTCGCCACCCTCACCATCCAAGGCATCCGGTTTGAGGACAATGGCATCTACTTCTGTCA  
GCAGAAGTGCAACAACACCTCGGAGGTCTACCAGGGCTGCGGCACAGAGCTGCGAGTCATGGGATTGAGCACCTTGG  
CACAGCTGAAGCAGAGGAACACGCTGAAGGATGGTATCATCATGATCCAGACGCTGCTGATCATCCTCTTCATCATC  
GTGCCTATCTTCTGCTGCTGGACAAGGATGACAGCAAGGCTGGCATGGAGGAAGATCACACCTACGAGGGCCTGGA  
CATTGACCAGACAGCCACCTATGAGGACATAGTGACGCTGCGGACAGGGGAAGTGAAGTGGTCTGTAGGTGAGCACC  
CAGGCCAGGAGTGAGAGCCAGGTCGCCCCATGACCTGGGTGCAGGCTCCCTGGCCTCAGTGACTGCTTCGGAGCTGC  
CTGGCTCATGGCCCAACCCCTTTCTGGACCCCCAGCTGGCCTCTGAAGCTGGCCCACCAGAGCTGCCATTTGTCT  
CCAGCCCCTGGTCCCCAGCTCTTGCCAAAGGGCCTGGAGTAGAAGGACAACAGGGCAGCAACTTGGAGGGAGTTCTC  
TGGGGATGGACGGGACCCAGCCTTCTGGGGGTGCTATGAGGTGATCCGTCCCCACACATGGGATGGGGGAGGCAGAG  
ACTGGTCCAGAGCCCGCAAATGGACTCGGAGCCGAGGGCCTCCCAGCAGAGCTTGGGAAGGGCCATGGACCCAACTG  
GGCCCCAGAAGAGCCACAGGAACATCATTCTCTCCCGCAACCACTCCCACCCCAGGGAGGCCCTGGCCTCCAGTGC  
CTTCCCCCGTGGAATAAACGGTGTGTCTGAGAAACCA

**FIGURE 63**

**FIGURE 64**

CCGTTCCGCGCTCTGGCGGCTCCTCCCGGGCGATGCCTCCGCTCTGGGCCCTGCTGGCCCTCGGCTGCCTGCGGTTC  
GGCTCGGCTGTGAACCTGCAGCCCCAACTGGCCAGTGTGACTTTCGCCACCAACAACCCACACTTACCACTGTGGC  
CTTGAAAAGCCTCTCTGCATGTTTGACAGCAAAGAGGCCCTCACTGGCACCCACGAGGTCTACCTGTATGTCCTGG  
TCGACTCAGCCATTTCCAGGAATGCCTCAGTGCAAGACAGCACCAACACCCCACTGGGCTCAACGTTCTACAAACA  
GAGGGTGGGAGGACAGGTCCCTACAAAGCTGTGGCCTTTGACCTGATCCCCTGCAGTGACCTGCCCAGCCTGGATGC  
CATTGGGGATGTGTCCAAGGCCTCACAGATCCTGAATGCCTACCTGGTCAGGGTGGGTGCCAACGGGACCTGCCTGT  
GGGATCCCAACTTCCAGGGCCTCTGTAACGCACCCCTGTTCGGCAGCCACGGAGTACAGGTTCAAGTATGTCCTGGTC  
AATATGTCCACGGGCTTGGTAGAGGACCAGACCCTGTGGTCGGACCCCATCCGCACCAACCAGCTCACCCCATACTC  
GACGATCGACACGTGGCCAGGCCGGCGGAGCGGAGGCATGATCGTCATCACTTCCATCCTGGGCTCCCTGCCCTTCT  
TTCTACTTGTGGGTTTTGCTGGCGCCATTGCCCTCAGCCTCGTGGACATGGGGAGTTCTGATGGGGAAACGACTCAC  
GACTCCCAAATCACTCAGGAGGCTGTTCCCAAGTCGCTGGGGGCCTCGGAGTCTTCTACACGTCCGTGAACCGGGG  
GCCGCCACTGGACAGGGCTGAGGTGTATTCCAGCAAGCTCCAAGACTGAGCCCAGCACCAACCCCTGGGCAGCAGCAT  
CCTCCTCTCTGGCCTTGCCCCAGGCCCTGCAGCGGTGGTTGTCACACCCTGACTTCAGGGAAGGTGAAACAGGGCTT  
GTCCCTCCAACCTGCAGGAAAACCCCTAATAAAATCTTCTGATGAGTTCTAAAAAAAAA

**FIGURE 65**

TCTCTGACCACCGGTGCATGCAGCCCCTGTCACATACCGCCTGCTTGCTCAAATCAATCATGACCCTTTCATGTGAA  
ATCTTTTAGTATTGTGAGCCCTTAAAAGGGACGGAAATTGTGCATACGTGGAGCTCGGATTTTAAGGCAGTAGCTGCC  
CGATGCTCCCAGCTGAATAAAGCCCTTCCTTCTACAATTTGGTGTCTGAGGGGTTTTGTCTGCGGCTCGTCCTGCTA  
CATTTCTTGGTTCCCTGACCGGGAAGCAAGGTGACTGACAGACGGCCGAGGCAGCCCCCTTAGGCGGCTTAAGCCTGC  
CCTGTGGAGCATCCCTGCGGGGGACTCCGGCCAGCCTGAGTGACGGATCCAAAGAGTGCTCCCGGTAGGAAATTG  
CCCCGGTGGAACGCCTCGCCAGAGCAGCGTGTAGCAGGCCCCGCGGAGGATTAACACAGTGGCTGAACACCGGGAA  
GGAAGTGGCACTTGGAGTCCAGACATCTGAAACTTGACTGGGAGCTGTACGTGGATGGGAGCAGCTTCACCAACCCC  
TGCAAAGTGACTCTGAAGAAGACGACAAGCCCTGCTCCAGTCACACCCGGAAGCTGACTGGTCCACGCACGGCCGAA  
GCATGAGGAAACTCATCGCAGGACTCATTTTTCTTAAATTTTGGACTTATACAGTAAGGGCTTCAACTGACCTTCCT  
CAGACTGAGAACTGTTTCCAGTATATACATCAAGTCACTGAGATCTCCAGCACCTGCCGGTGGCACTACTGAGAGA  
CGAGGTGCCAGGGTGGTTCTGAAAGTGCCTGAGCCCCAACTTATCAGCAAGGAGCTCATCATGCTGACAGAAGTCA  
TGGAGGTCTGGCATGGCTTAGTGATCGCGGTGGTGTCCCTCTTCCTGCAGGCCTGCTTCCTCACCGCCATCAACTAC  
CTGCTCAGCAGGCACATGGCCCCACAAGAGTGAACAGATACTGAAAGCGGCCAGTCTCCAGGTTCCCAGGCCAGCCC  
TGGCCACCATCATCCACCTGCTGTCAAAGAGATGAAGGAGACTCAGACAGAGAGAGACATCCCAATGTCTGATTCCC  
TTTACAGGCATGACAGCGACACACCCTCAGATAGCTTGATAGCTCCTGCAGTTCGCCTCCTGCCTGCCAGGCCACA  
GAGGATGTGGATTACACACAAGTCGTCTTTTCTGACCCTGGAGAACTAAAATGACTCCCCGCTGGACTATGAGAACA  
TAAAGGAAATCAGATTATGTCAATGTCAATCCAGAAAGACACAAGCCCAGTTTCTGGTATTTTGTCAACCCTGCT  
TCTTGTCTGAGCCAGCGGAATTATGATCAAGTGGCCATGTGAATTCCAAATATTTTTTAAATGGGGTCCAGTTCTCT  
ATGGNTTCTTANAATTTAATTTTGTAGGGGNAANTGCCATTTTNCCCCTTTTAAACAANGNTTGGGGNTAAAAGN  
TTTTTNGGGCCA

**FIGURE 66**

AAACTTTTCAGCGGCTGGGTAGCAGCACGTCTCTTGCTCCTCAGGGCCACTGCCAGGCTTGCCGAGTCCTGGGACT  
 GCTCTCGCTCCGGCTGCCACTCTCCCGCGCTCTCCTAGCTCCCTGCGAAGCAGGATGGCCGGGACCGTGCGCACCGC  
 GTGCTTGGTGGTGGCGATGCTGCTCAGCTTGGAATTTCCCGGGACAGGCGCAGCCCCGCCGCCGCCGCCGGACGCCA  
 CCTGTACCAAGTCCGCTCCTTCTTCCAGAGACTGCAGCCCGGACTCAAGTGGGTGCCAGAACTCCCGTGCCAGGA  
 TCAGATTTGCAAGTATGTCTCCCTAAGGGCCCAACATGCTGCTCAAGAAAGATGGAAGAAAAATACCAACTAACAGC  
 ACGATTGAACATGGAACAGCTGCTTCAGTCTGCAAGTATGGAGCTCAAGTTCTTAATTATTGAGAATGCTGCGGTTT  
 TCCAAGAGGCCTTTGAAATTGTTGTTGCCATGCCAAGAATAACCAATGCCATGTTCAAGAACAATAACCAAGC  
 CTGACTCCACAAGCTTTTGAGTTTGTGGGTGAATTTTTCACAGATGTGTCTCTTACATCTTGGGTCTGACATCAA  
 TGTAGATGACATGGTCAATGAATTGTTTGACAGCCTGTTTCCAGTCATCTATACCCAGCTAATGAACCCAGGCTGCG  
 CTGATTGAGCCTTGGACATCAATGAGTGCCTCCGAGGAGCAAGACGTGACCTGAAAGTATTTGGGAATTTCCCAAG  
 CTTATTATGACCCAGGTTTCCAAGTCACTGCAAGTCACTAGGATCTTCTTCAGGCTCTGAATCTTGAATTGAAGT  
 GATCAACACAACCTGATCACCTGAAGTTCAGTAAGGACTGTGGCCGAATGCTCACCAGAATGTGGTACTGCTCTTACT  
 GCCAGGGACTGATGATGGTTAAACCCTGTGGCGGTTACTGCAATGTGGTCATGCAAGGCTGTATGGCAGGTGTGGTG  
 GAGATTGACAAGTACTGGAGAGAATACATTCTGTCCCTTGAAGAACTTGTAATGGCATGTACAGAATCTATGACAT  
 GGAGAACGTACTGCTTGGTCTCTTTTCAACAATCCATGATTCTATCCAGTATGTCCAGAAGAATGCAGGAAAGCTGA  
 CCACCACTATTGGCAAGTTATGTGCCATTCTCAACAACGCCAATATAGATCTGCTTATTATCCTGAAGATCTCTTT  
 ATTGACAAGAAAGTATTAAGAGTTGCTCATGTAGAACATGAAGAAACCTTATCCAGCCGAAGAAGGGAACTAATTCA  
 GAAGTTGAAGTCTTTTCATCAGCTTCTATAGTGCTTTCCTGGCTACATCTGCAGCCATAGCCCTGTGGCGGAAAACG  
 ACACCCCTTGCTGGAATGGACAAGAACTCATGGAGAGATACAGCCAAAAGGCAGCAAGGAATGGAATGAAAAACCAG  
 TTCAATCTCCATGAGCTGAAAATGAAGGGCCCTGAGCCAGTGGTCAGTCAAATTATTGACAACTGAAGCACATTAA  
 CCAGCTCCTGAGAACCATGTCTATGCCCCAAGGTAGAGTTCTGGATAAAAACCTGGATGAGGAAGGGTTTGAAAGTG  
 GAGACTGCGGTGATGATGAAGATGAGTGCATTGGAGGCTCTGGTGATGGAATGATAAAAGTGAAGAATCAGCTCCGC  
 TTCCTTGCAAGAACTGGCCTATGATCTGGATGTGGATGATGCGCCTGGAAACAGTCAGCAGGCAACTCCGAAGGACAA  
 CGAGATAAGCACCTTTCACAACCTCGGGAACGTTTATTCCCGCTGAAGCTTCTCACCAGCATGGCCATCTCGGTGG  
 TGTGCTTCTTCTTCTGGTGCACTGACTGCCTGGTGCCAGCACATGTGCTGCCCTACAGCACCCCTGTGGTCTTCT  
 CGATAAAGGGAACCACTTTCTTATTTTTTTCTATTTTTTTTTTTTTTTGTTATCCTGTATACCTCCTCCAGCCATGAAG  
 TAGAGGACTAACCATGTGTTATGTTTTCGAAAATCAAATGGTATCTTTTGGAGGAAGATACATTTTAGTGGTAGCAT  
 ATAGATTGTCCTTTTGCAAAGAAAGAAAAAAACCATCAAGTTGTGCCAAATTATTCTCCTATGTTGGCTGCTAGA  
 ACATGGTTACCATGTCTTCTCTCTCACTCCCTCCCTTTCTATCGTTCTCTCTTGCATGGATTCTTTGAAAAAA  
 ATAAATTGCTCAAATA

**FIGURE 67**

GCGGAACACCGGCCCCGCGTCGCGGCAGCTGCTTCACCCCTCTCTCTGCAGCC**ATG**GGGCTCCCTCGTGGACCTCTC  
 GCGTCTCTCCTCCTTCTCCAGGTTTGTGGCTGCAGTGCAGCGGCTCCGAGCCGTGCCGGGCGGTCTTCAGGGAGGC  
 TGAAGTGACCTTGGAGGCGGGAGGCGCGGAGCAGGAGCCCGGCCAGGCGCTGGGGAAGTATTCATGGGCTGCCCTG  
 GGCAAGAGCCAGCTCTGTTTAGCACTGATAATGATGACTTCACTGTGCGGAATGGCGAGACAGTCCAGGAAAGAAGG  
 TCACTGAAGGAAAGGAATCCATTGAAGATCTTCCCATCCAAACGTATCTTACGAAGACACAAGAGAGATTGGGTGGT  
 TGCTCCAATATCTGTCCCTGAAAATGGCAAGGGTCCCTTCCCCCAGAGACTGAATCAGCTCAAGTCTAATAAAGATA  
 GAGACACCAAGATTTTCTACAGCATCACGGGGCCGGGGGAGACAGCCCCCTGAGGGTGTCTTCGCTGTAGAGAAG  
 GAGACAGGCTGGTTGTTGTTGAATAAGCCACTGGACCGGGAGGAGATTGCCAAGTATGAGCTCTTTGGCCACGCTGT  
 GTCAGAGAATGGTGCCTCAGTGGAGGACCCCATGAACATCTCCATCATCGTGACCGACCAGAATGACCACAAGCCCCA  
 AGTTTACCCAGGACACCTTCCGAGGGAGTGTCTTAGAGGGAGTCTTACCAGGTACTTCTGTGATGCAGGTGACAGCC  
 ACAGATGAGGATGATGCCATCTACACCTACAATGGGGTGGTTGCTTACTCCATCCATAGCCAAGAACCAAGGACCC  
 ACACGACCTCATGTTACAATTACCGGAGCACAGGCACCATCAGCGTCATCTCCAGTGGCCTGGACCGGGAAAAAG  
 TCCCTGAGTACACACTGACCATCCAGGCCACAGACATGGATGGGGACGGCTCCACCACCAGGCAGTGGCAGTAGTG  
 GAGATCCTTGATGCCAATGACAATGCTCCCATGTTTGACCCCCAGAAGTACGAGGCCCATGTGCCTGAGAATGCAGT  
 GGGCCATGAGGTGCAGAGGCTGACGGTCACTGATCTGGACGCCCCCAACTCACCAGCGTGGCGTGCCACCTACCTTA  
 TCATGGGCGGTGACGACGGGGACCAATTTTACCATCACCAACCCACCTGAGAGCAACCAGGGCATCCTGACAACAGG  
 AAGGGTTTGGATTTTGAGGGCAAAAACCAGCACACCCTGTACGTTGAAGTGACCAACGAGGCCCCCTTTTGTGCTGAA  
 GCTCCCAACCTCCACAGCCACCATAGTGGTCCACGTGGAGGATGTGAATGAGGCACCTGTGTTTGTCCACCCCTCCA  
 AAGTCGTTGAGGTCCAGGAGGGCATCCCCACTGGGGAGCCTGTGTGTGTCTACACTGCAGAAGACCCGTACAAGGAG  
 AATCAAAAGATCAGCTACCGCATCCTGAGAGACCCAGCAGGGTGGCTAGCCATGGACCCAGACAGTGGGCAGGTGAC  
 AGCTGTGGGCGGTGACGACGGGGACCAATTTTACCATCACCAACCCACCTGAGAGCAACCAGGGCATCCTGACAACAGG  
 ACAATGGAAGCCCTCCACCACTGGCACGGGAACCCCTTCTGCTAACACTGATTGATGTCAACGACCATGGCCCCAGTC  
 CCTGAGCCCCGTGAGATCACCATCTGCAACCAAGCCCTGTGCGCCACGTGCTGAACATCACGGACAAGGACCTGTC  
 TCCCCACACCTCCCCTTTCCAGGCCAGCTCACAGATGACTCAGACATCTACTGGACGGCAGAGGTCAACGAGGAAG  
 GTGACACAGTGGTCTTGTCCCTGAAGAAGTTTCTGAAGCAGGATACATATGACGTGCACCTTTCTCTGTCTGACCAT  
 GGCAACAAAGAGCAGCTGACGGTGTATCAGGGCCACTGTGTGCGACTGCCATGGCCATGTGCAAAACCTGCCCTGGACC  
 CTGGAAAGGAGGTTTTCATCCTCCCTGTGCTGGGGGCTGTCTGGCTCTGCTGTTCTCCTGCTGGTGTGCTTTTGT  
 TGGTGAGAAAGAAGCGGAAGATCAAGGAGCCCCCTCTACTCCCAGAAGATGACACCCGTGACAACGTCTTCTACTAT  
 GGCGAAGAGGGGGTGGCGAAGAGGACCAGGACTATGACATCACCCAGCTCCACCGAGGTCTGGAGGCCAGGCCGGA  
 GGTGGTTCTCCGCAATGACGTGGCACCACCATCATCCCGACCCCATGTACCGTCTTAGGCCAGCCAACCCAGATG  
 AAATCGGCAACTTTATAATTGAGAACCTGAAGGCGGCTAACACAGACCCACAGCCCCGCCCTACGACACCCCTCTTG  
 GTGTTGACTATGAGGGCAGCGGCTCCGACGCCGCGTCCCTGAGCTCCCTCACCTCCTCCGCTCCGACCAAGACCA  
 AGATTACGATTATCTGAACGAGTGGGGCAGCCGCTTCAAGAAGCTGGCAGACATGTACGGTGGCGGGGAGGACGACT  
**AG**CGGCGCTGCCTGCAGGGCTGGGGACCAACGTGAGGCCACAGAGCATCTCCAAGGGGTCTCAGTTCCCCCTTCAG  
 CTGAGGACTTCGGAGCTTGTGAGGAAGTGGCCGTAGCAACTTGGCGGAGACAGGCTATGAGTCTGACGTTAGAGTGG  
 TTGCTTCCTTAGCCTTTTCAGGATGGAGGAATGTGGGCAGTTTGACTTCAGCACTGAAAACCTCTCCACCTGGGCCAG  
 GGTGCTCAGAGGCCAAGTTTCCAGAAGCCTCTTACCTGCCGTAAAATGCTCAACCTGTGTCCTGGGCCTGGGCC  
 TGCTGTGACTGACCTACAGTGGACTTTCTCTCTGGAATGGAACCTTCTTAGGCCTCCTGGTGCAACTTAATTTTTTT  
 TTTTAATGCTATCTTCAAAACGTTAGAGAAAGTTCTTCAAAAGTGCAGCCAGAGCTGCTGGGCCCCACTGGCCGTCC  
 TGCATTTCTGGTTTCCAGACCCCAATGCCTCCCATTCGGATGGATCTCTGCGTTTTTATACTGAGTGTGCCTAGGTT  
 GCCCTTATTTTTTATTTTCCCTGTTGCGTTGCTATAGATGAAGGTGAGGACAATCGTGTATATGTACTAGAACTT  
 TTTTATTAAAGAAA



**FIGURE 68**

GCGCCTTGCCCGGGCCCCGCGGGCCTCAGGCCCGGGGACCCTCAGCGCTACCTTTTGCCTCCGGCTCTGGGACTG  
CTCGTGGCCGCGGGCGTGGCCGGCGCTGCGCTCTTGCTGGTCCACGTGCGCCGCCGTGGCCACTCCCAGGATGCTGG  
GTCTCGCTTGCTGGCTGGGACCCCGGAGCCGTCAGTCCACGCACTCCCGGATGCACTCAACAACCTAAGGACGCAGG  
AGGGTTCCGGGGATGGTCCGAGCTCGTCCGTAGATTGGAATCGCCCTGAAGATGTAGACCCTCAAGGGATTTATGTC  
ATATCTGCTCCTTCCATCTACGCTCGGGAGGTAGCGACGCCCCCTTTCCCCCGCTACACACTGGGCGCGCTGGGCA  
GAGGCAGCACCTGCTTTXX  
XXXXXXXXXXXXCGGGCGTGGCCGGCGCTGCGCTCTTGNTGGTCCANGTGCNGCCGTGGCCAATCNCAGGATGC  
TGGGTCNCGCTTNCTGGTTNGGACCCCGNGCCGTNAGTCCACNCACTCCNNGATGCACTCAACAACCTAAGGACGC  
AGGAGGGTTCCCGGGGATGGTCCGAGCTCGTCCGTAGATTGGAATCGCCCTGAAGATGTAGACCCTCACAGGGAGTG  
TATGTAATXXTCCGCACGTGGAGTCAGAG  
CGTGGATTTTGTANNTGCTNGGTGGTGCCAGTCTCTGCCCCNGAGGCTTTGGANTTCAATCTTGAAGGGGTGTNC  
TGGGGAACTTTACTGTTGCAAGTTGTAAATAATGGTTNNTTATATCGTNTTTTTTCGTCACCCCATCTCTGATAGA  
AACACCTNTAAAGGNTATTATTGTGAGTCAAAAAA

**FIGURE 69**

GCGGCGACTGCGGCGACCGCGGGACGGCGAGAGGCACGCGGCGGGAGGGGACCGGAATCCGCAGCTCCGGCCGCGCC  
 ATGGACGGCAACGACAACGTGACCCTGCTCTTCGCCCTCTGCTGCGGGACAACCTACACCCTGGCGCCCAATGCCAG  
 CAGCCTGGGCCCCGGCACGGACCTCGCCCTCGCCCTGCCTCCAGCGCCGGCCCCGGCCCTGGGCTCAGCCTCGGGC  
 CGGGTCCGAGCTTCGGCTTCAGCCCCGGCCCCACTCCGACCCCGGAGCCACGACCAGCGGCCTCGCGGGCGGCGCG  
 GCGAGCCACGGCCCTTCCCCGTTCCCTCGGCCCTGGGCGCCCCACGCGCTCCCGTTCTGGGACACGCCGCTGAACCA  
 CGGGCTGAACGTGTTTCGTGGGCGCCGCCCTGTGCATCACCATGCTGGGCCTGGGCTGCACGGTGGACGTGAACCACT  
 TCGGGGCGCACGTCCGTGCGCCCGTGGGCGCGCTGCTGGCAGCGCTCTGCCAGTTCGGCCTCCTGCCGCTGCTGGCC  
 TTCCTGCTGGCCCTCGCCTTCAAGCTGGACGAGGTGGCCGCCGTGGCGGTGCTCCTGTGTGGCTGCTGTCCCGGCGG  
 CAATCTCTCCAATCTTATGTCCCTGCTGGTTGACGGCGACATGAACCTCAGCATCATCATGACCATCTCCTCCACGC  
 TTCTGGCCCTCGTCTTGATGCCCCTGTGCCTGTGGATCTACAGCTGGGCTTGATCAACACCCCTATCGTGCAGTTA  
 CTACCCCTAGGGACCGTGACCCTGACTCTCTGCAGCACTCTCATACCTATCGGGTTGGGCGTCTTCATTCGCTACAA  
 ATACAGCCGGGTGGCTGACTACATTGTGAAGTTTCCCTGTGGTCTCTGCTAGTGACTCTGGTGGTCCCTTTTCATAA  
 TGACCGGCACTATGTTAGGACCTGAACCTGCTGGCAAGTATCCCTGCAGCTGTTTATGTGATAGCAATTTTATGCCT  
 TTGGCAGGCTACGCTTCAGGTTATGGTTTAGCTACTCTCTCCATCTTCCACCCAACGCAAGAGGACTGTATGTCT  
 GGAAACAGGTAGTCAGAATGTGCAGCTCTGTACAGCCATTCTAAACTGGCCTTTCACCGCAATTCATAGGAAGCA  
 TGTACATGTTTCCTTTGCTGTATGCACTTTTCCAGTCTGCAGAAGCGGGATTTTTGTTTTAATCTATAAAATGTAT  
 GGAAGTGAAATGTTGCACAAGCGAGATCCTCTAGATGAAGATGAAGATACAGATATTTCTTATAAAAACTAAAAGA  
 AGAGGAAATGGCAGACACTTCCTATGGCACAGTGAAAGCAGAAAATATAATAATGATGGAAACCGCTCAGACTTCTC  
 TCTAAATGTGGAGATACACAGGAGCTTCTATCTTGCTGAAATATTGCTTCATATTTATAGCCTGTGGTAGTGCACAT  
 GGTAAACATAAAAGATAACACTGGTTCACATCATACATGTAACAATTCTGATCTTTTTAAGGTTCACTGGTGTATTA  
 ACCAAACGTTGTCACAAATTACAAATCAATGCTGTAATATAATTTGCACCTGGAATGGCTAACGTGAAGCCTGAATT  
 AAATGTGGTTTTTAGTTTTTACCATCACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 70**

CGGCCAGCACACCCCGGCACCTCCTCTGCGGCAGCTGCGCCTCGCAAGCGCAGTGCCGCAGCGCACGCCGGAGTGGC  
 TGTAGCTGCCTCGGCGCGGCTGCCGCCCTGCGCGGGCTGTGGGCTGCGGGCTGCGCCCCGCTGCTGGCCAGCTCTG  
 CACGGCTGCGGGCTCTGCGGCGCCCGGTGCTCTGCAACGCTGCGGCGGGCGGCATGGGATAACGCGGCC**ATG**GTGCG  
 CCGAGATCGCCTCCGCAGGATGAGGGAGTGGTGGGTCCAGGTGGGGCTGCTGGCCGTGCCCTGCTTGCTGCGTACC  
 TGCACATCCCACCCCTCAGCTCTCCCCTGCCCTTCACTCATGGAAGTCTTCAGGCAAGTTTTTCACTTACAAGGGA  
 CTGCGTATCTTCTACCAAGACTCTGTGGGTGTGGTTGGAAGTCCAGAGATAGTTGTGCTTTTACACGGTTTTTCCAAC  
 ATCCAGCTACGACTGGTACAAGATTTGGAAGGGTCTGACCTTGAAGTTTCATCGGGTGATTGCCCTTGATTTCTTAG  
 GCTTTGGCTTCAGTGACAAACCGAGACCACATCACTATTCCATATTTGAGCAGGCCAGCATCGTGGAAGCGCTTTTG  
 CGGCATCTGGGGCTCCAGAACCGCAGAATCAACCTTCTTTCTCATGACTATGGAGATATTGTTGCTCAGGAGCTTCT  
 CTACAGGTACAAGCAGAATCGATCTGGTCGGCATAACCATAAAGAGTCTCTGTCTGTCAAATGGAGGTATCTTTCCTG  
 AGACTCACCGTCCACTCCTTCTCCAAAAGCTACTCAAAGATGGAGGTGTGCTGTCAACCATCCTCACACGACTGATG  
 AACTTCTTTGTATTCTCTCGAGGTCTCACCCAGTCTTTGGGCCGTATACTCGGCCCTCTGAGAGTGAGCTGTGGGA  
 CATGTGGGCAGGGATCCGCAACAATGACGGGAACCTAGTCATTGACAGTCTCTTACAGTACATCAATCAGAGGAAGA  
 AGTTTCAAGGCGCTGGGTGGGAGCTCTTGCTCTGTAACATATCCCATTCATTTTATCTATGGGCCATTGGATCCT  
 GTAAATCCCTATCCAGAGTTTTTGGAGCTGTACAGGAAAACGCTGCCGCGGTCCACAGTGTGATTCTGGATGACCA  
 CATTAGCCACTATCCACAGCTAGAGGATCCCATGGGCTTCTTGAATGCATATATGGGCTTCATCAACTCCTTCT**TGAG**  
 CTGGAAGAGTAGCTTCCCTGTATTACCTCCCCTACTCCCTTATGTGTTGTGTATTCCACTTAGGAAGAAATGCCCA  
 AAAGAGTCTTGCCATCAAACATAATTCTCTCACAAAGTCCACTTTACTCAAATTGGTGAACAGTGTATAGGAAGA  
 AGCCAGCAGGAGCTCTGACTAAGGTTGACATAATAGTCCACCTCCCATTACTTTGATATCTGATCAAATGTATAGAC  
 TTGGCTTTGTTTTTTGTGCTATTAGGAAATTCTGATGAGCATTACTATTCACTGATGCAGAAAGACGTCTTTTGA  
 TAAAAGACTTTTTTTTAACTTTGGACTTCTCTGAAATATTTAGAAGTGCTAATTTCTGGCCCCACCCCAACAGGA  
 ATTCTATAGTAAGGAGGAGGAGAAGGGGGGCTCCTTCCCTCTCCTCGAATGACGTTATGGGCACATGCCTTTTAAAA  
 GTTCTTTAAGCAACACAGAGCTGAGTCCTCTTGTACATACCTTTGGATTAGTGTTTCATCAGCTGTTTTTAGTTAT  
 AAACATTTTGTAAAAATAGATATTGGTTTAAATGATACAGTATTTTAGGTATGATTTAAGACTATGATTTACCTATA  
 CATTATATATATTTTATAAAGATACTAAACCAGCATAACCCTTACTCTGCCAGAGTAGTGAAGCTAATTAAACACGTT  
 TGGTTTCTGAATAAATTGAACTAAATCCAAACTATTTTCTAAATCACAGGACATTAAGGACCAATAGCATCTGTGC  
 CAGAGATGTACTGTTATTAGCTGGGAAGACCAATTCTAACAGCAAATAACAGTCTGAGACTCCTCATACCTCAGTGG  
 TTAGAAGCATGTCTCTCTTGAGCTACAGTAGAGGGGAAGGGATTGTTGTGTAGTCAAGTCACCATGCTGAATGTACA  
 CTGATTCCCTTTATGATGACTGCTTAACTCCCCACTGCCTGTCCAGAGAGGCTTTCCAATGTAGCTCAGTAATTCCT  
 GTTACTTTACAGACAGGAAAGTTCCAGAACTTTAAGAACAACTCTGAAAGACCTATGAGCAAATGGTGCTGAATA  
 CTTTTTTTTTAAAGCCACATTTTATTGTCTTAGTCAAAGCAGGATTATTAAGTGATTATTTAAATTCGTTTTTTTA  
 AATTAGCAACTTCAAGTATAACAACCTTTGAACTGGAATAAGTGTATTTTCTATTATAAATAAATGAATTGTGACA  
 AAAAAAAAAACCG

**FIGURE 71A**

CGGGTGGACAAGTCACCTGTCTAACTGTGGTGAGAGCAACAGGCCTCCAAAGGAAAGAAGTTGTTTCCGAGTTTGTG  
 ACTGGCACAGTGACCTCTTTTCAGTGGGAGGTTTCTGACTGGCACCACCTGTGTGCTTGTTCCTTACGCTCGCGGTGAA  
 GTCAAGCCTCGGACTGCAGAGTGTGTGACGGCTCAGCATGGACTGCAGCACC GGATGGTGCGCTGCATTCAAGAGCT  
 GAACCGAAGTGTGGTTGCAAATGAAATATGCGAACACTTTGCCCTTCAGCCTCCTACAGAACAGGCTTGCCCTCATTC  
 CTTGTCCCCGGGATTGTGTAGTATCTGAGTTCTTACCATGGTCCAACCTGTAGCAAGGGATGTGGGAAGAAATTCGAG  
 CATAGAAGTTCGCGGGTCATAGCTCCCCCTCTCTTTGGTGGTTTGAATGTCCAAATCTGACTGAGTCAAGAGCCTG  
 TGATGCTCCCATTTCTGTCTCTTGGGGAAGAGGAATATACATTTAGCCTTAAGGTTGGACCATGGAGTAAATGCA  
 GACTGCCTCATCTTAAAGAAATTAATCCAAGCGGAAGAAGTGTCTGGATTCTAACTCTGATTCAAATGAGCGAGTC  
 ACCTTTAAACATCAAAGTTACAAAGCACATCATCATTCGAAGTCTTGGGCAATAGAGATAGGTTATCAAACCCGGCA  
 GGTTTCGTGTACAAGAAGTGTGACAAATGCTATGTTAAGCCTTTGCCTTCAAGATTCTTCCCATTGACTGTTT  
 AGTCCTGCATCATGCCCAAAGACTGTGAAACCTCCCAGTGGTCCCTCCTGGAGCCCCTGCTCCAAGACATGCCGTTCA  
 GGGAGTCTCTTGGCAGGATTTAGGAGCAGGAGCCGGAACGTGAAGCACATGGCTATTGGAGGTGGAAAGGAGTGTCC  
 TGAACCTCTTGAGAAAGAGGCCTGCATTGTTGAAGGAGAAGTCTGAGCAATGTCCAGGTATTCTGGAGAACTT  
 CTGAATGGAAAGAATGCCAAGTCTCTCTCCTCCTCGAGCAGCAGGATCCCCACTGGCATGTGACGGGACCCGTGTGT  
 GGCGGTGGGATCCAGACCCGGGAGGTGTACTGTGCCAGAGCGTACCAGCAGCTGCCGCACTGAGGGCCAAGGAAGT  
 CTCTAGACCTGTGGAAAAGGCATTATGTGTGGGACCCGCCCTTGCCTCTCAGCTCTGCAATATCCCTTGCTCTA  
 CGGACTGCATAGTATCTTCTGGTCAAGCTGGGCGCTGTGCATCCATGAAAAGTGTATGAACCTCAGGGGAAAAAA  
 GGATTTAGAACGAGGCAGCGCCATGTCTCATGGAATCTACAGGGCCTGCAGGGCATTGCCCTCATTTGGTGGAGTC  
 TGTTCCCTGTGAGGATCCAATGTGTACCGATGGCTGGCATCAGAAGGGATCTGTTTCCCTGATCATGAAAATGTG  
 GCCTGGGACATCGTATTCTGAAGGCCGTCTGCCAGAATGACCGCGGAGAAGATGTATCAGGGAGTCTTTGCCAGTT  
 CCCCCTCCTCTGAGAGGAAGTCTTGTGAAATTCCTGCCAATGGACTGTGTGCTGAGCGAGTGGACGAGTGGTC  
 ATCCTGTTCCAGTCTGTTCAAATAAAAACTCAGATGGGAAACAGACCAGGTCAAGAACTATCCTGGCACTGGCTG  
 GGGAAAGTGGAAAGCCATGTCCCCCTAGTCAGGCTCTCCAAGAGCATCGTTTGTGTAATGACCATTCTGTATGCAG  
 CTTCACTGGGAGACATCGCCTTGGGGCCCTTGTCTGAGGACACATTGGTAACTGCCCTTAATGCAACCATTGGCTG  
 GAATGGAGAAGCCACGTGTGGTGTAGGCATTCAAGTCTCGAGAGTCTTCTGTGTCAAGAGTCACGTGGGACAAGTAA  
 TGACCAAAAGATGTCCAGATTCTACTCGACCTGAAACTGTGCGCCCTGTTTTCTCCCATGCAAAAAGACTGTATT  
 GTGACTGCTTTCAGTGAGTGGACACCCCTGCCAAGGATGTGCCAAGCAGGAAATGCCACAGTAAAAACAGTCTCGATA  
 CAGAATCATCATCCAAGAAGCAGCCAATGGAGGCCAGGAATGCCAGATACCTTATATGAGGAGAGAGAGTGTGAAG  
 ATGTTTCCCTGTGTCTGTATATCGGTGGAAGCCACAGAAATGGAGCCCTTGCATCTTAGTGCCAGAGTCTGTCTGG  
 CAGGGAATAACGGGCAGCAGTGAAGCCTGTGGAAGGGGTACAAACAAGAGCTGTCTCATGCATCTCTGATGACAA  
 CCGGTGAGCAGAAATGATGGAATGCCCAAGCAGACAAACGGCATGCCTCTCCTTGTGCAAGAAATGCACAGTCCCAT  
 GTCGAGAAGACTGCACCTTCACTGCTTGGTCCAAGTTTACGCCCTGCTCCACGAAGTGTGAAGCCACAAAAAGTAGG  
 CGGCGACAGCTCACAGGGAAAAGCAGAAAGAAGGAGAAATGCCAGGATTCTGACCTTTACCCTCTAGTGGAGACAGA  
 ACTATGTCTTGTGATGAATTTATATCCCAACCTTATGAAACTGGTCAGATTGCATTCTTCCAGAAGGCAGAAGGG  
 AGCCTCACCGAGGACTGCGGGTACAAGCAGACAGCAAGAATGTGGAGAAGGCCTGCGCTTTCGAGCAGTAGCCTGT  
 TCTGATAAAAAATGGAAGACCTGTTGACCCCTCCTTCTGCAGCAGCTCTGGTTACATTCAAGAAAAATGTGTCAATTC  
 CTGCCCATTTGATTGCAAGTTAAGCGATTGGTCTAGTTGGGGGTCTTGCAAGTTCATCTTGTGGAATTGGAGTGAGAA  
 TTCGATCCAAATGGCTAAAAGAAAAACCTTACAATGGAGGACGACCATGTCCCAACTGGATCTCAAGAATCAGGCT  
 CAGGTACATGAGGCAGTCCCATGTTACAGTGAGTGCAATCAGTATTCCTGGGTGTAGAACACTGGTCTTCATGCAA  
 AATCAACAATGAGCTGAGGTCCCTGCGCTGTGGAGGAGGAACACAATCTAGGAAAATCAGATGTGTGAATACTGCGG  
 ATGGTGAAGGTGGAGCAGTGGATAGCAACCTGTGCAACCAGGATGAAATTCCTCCAGAAACCCAGTCCCTGTTCTCTT  
 ATGTGTCCCAATGAGTGTGTCTGTGAGTGGGGACTTTGGAGCAAATGCCACAGTCAATGCGATCCCCACACAAT  
 GCAGAGAAGAACTCGCCACCTGCTAAGACCATCACTGAACCTCAAGGACTTGTGCTGAAGACTCACAGGTGCAGCCTT  
 GCCTCCTGAATGAAAATTGCTTCCAGTTCAGTACAATCTAACAGAGTGGAGCACATGCCAGCTGAGTGAAAACGCA  
 CCCTGTGGTCAAGGCGTCAGGACCCGCTGCTAAGCTGTGTGTGCAAGTGTGGCAAGCCAGTCAGCATGGACCAATG  
 TGAGCAGCATAATTTGGAGAAGCCCCAGAGAATGAGCATTCCTTGCTTGGTGAATGCGTGGTCAACTGTGAGCTCT  
 CAGGGTGGACGGCTTGGACAGAGTGTTCACAGACCTGTGGCCATGGAGGTGCAATGAGCCGAGTCTGATTTATCATT  
 ATGCCAACCAAGGAGAAGGACGGCCATGCCCCACAGAGCTTACCCAGGAGAAAACCTGCCAGTGACCCCTGCTA  
 CAGCTGGGTCTTGGCAACTGGTCTGCATGTAAATTTGGAGGGTGGAGACTGTGGGGAAGGAGTTCAGATCCCGCAGCC  
 TTTCTGATGAGTCCACAGTGGTCAATATCTCATGCAGCTGGACGTGTGAGGATGCACTGTGTGGAGAAATGCCC  
 TTTACAGACAGCATCCTGAAGCAGCTGTGTTCTGTGCTTGGCCAGGAGACTGCCATTTAACAGAAATGGTCAGAGTG  
 GAGCACATGTGAATTAACCTGCATTGATGGAAGAAGCTTTGAGACTGTGGGCCGCCAGTCTAGATCAAG

**FIGURE 71B**

GACTTTTATAATTTCAGTCTTTTGAGAACCAAGACAGCTGCCCCCAACAGGTTCCTAGAAACACGCCCTTGTACAGGAG  
GCAAATGTTATCACTACACATGGAAAGCAAGTCTTTGGAACAATAACGAACGAACTGTATGGTGCCAGCGTTCAGAT  
GGCGTTAATGTCACAGGAGGCTGCTCCCCCTCAGGCCCGTCTGCTGCCATTTCGGCAGTGCATTCCAGCCTGCAGAAA  
ACCTTTCTCCTACTGTACACAGGGTGGAGTCTGTGGTTGTGAGAAGGGCTATACAGAGATAATGAGATCAAATGGTT  
TCCTGGATTACTGCATGAAAGTACCAGGCTCAGAGGATAAAAAAGCTGATGTGAAAAACCTTTCTGGGAAAAACAGA  
CCTGTGAATTCAAAAATACATGATATTTTTAAAGGATGGTCTCTTCAACCACTTGATCCAGATGGCCGAGTAAAAAT  
TTGGGTTTATGGCGTTTCAGGTGGCGCTTTTCTCATCATGATTTTCCTAATATTTACTTCCTACCTTGTTTGCAAGA  
AGCCAAAACCATCAAAGCACACCTCCCCAACAGAAGCCTCTGACCTTAGCCTACGATGGAGACTTAGACATGTA  
TCTGAAAAAGAAATCCAAATGTAGACATCAACTGCCTTAACCGCTTTCTCTTTGTAGCTCTCAGACTTCTCAGTTT  
TTTGAGGAATCTCAAGATGTGATATATTGGGCAGAATACAAATATTGCAAAAAGTAATATTGCCTCAACTTCATTTGG  
ACATGGAGTCAAGGATTATTAGGTCTGCCATTTTGTTCAGTTGTTTGTGGGTGTGTTTTATTTTTTTGGTTTTTC  
CCAAGGGACCTGAAAACCTTCTCTTCTGTTTGGAACTGGGAGGAAGAAAACATGATGGAATTTCCACAGACTTGA  
GTAAACTTGATCTTCAGCAGCATAATGACAATCCAGAGGAAAATACAGTCAAGGCATTTACTCTAAATGACGAGTCT  
GACACTGCATTGTTACGCACTATATTAGTGCAAAGTCTTTATTCTTCCCATACTTCAACACTGAGTTTTCTAGAGTT  
TACTTTGGTTTAAAGACTTTCAAATTGGATTGCCTATTTTTTCATGAACACAGAGAGAATGGATTACCATTTTCAGAAA  
TTCTCTGAGTTTTTAACCTTTAAATATTGTATTTTGTGTTTGTAGCCAGGGGATGATGGCGCTTCATGGGTTGCAGCT  
ACTGAAAATAGCAGCGTGTGTGTAATTGCTGGACTAGATGAAAGCTAGGTCATTTCTGAAGGGAATGTGTACTGAAT  
GTTAGAGGTACAAATGAAATATGTGGTTAAATTGGAGAATGAGGTAGATTATTTGATTACTAAAACGTATTTTAA  
CAAAACTTATCCATGTAGATATAGCATTAACCACACACAGTTGTAATTCAGTTTAAATGATGACAAACTCTGCTTTT  
GTAATTTCAATTTTCTTATCTGAATATTTATAAATCTCTTTCAAATTTAATTATCTGACCTCATTTAATATACAT  
CAACACCGATCCTGTTTGTACAAAGTCTTGCTTTTATAAGGTTTCAATAATATCTAAAACAACACATTAAAAAGCT  
GAGACCATTTTATGAAGATAATTGTTTGTAATCATAGGTGTTGAAAGTAAAAAGGTGCCATCTTGTGGTATTGACTT  
GTATTTATAACAAATAAACTGCTCAAGAGACTGC

**FIGURE 72A**

CCCACCTCGGCCACACTGCTTCGCTCCCCCTCCCCACCTTCAGCTGGCACCACGAAACAAGCCTTACCTCGTTGCAT  
 CTGCGAGGAGAGGTAGCAACAGCGAGCCTAGCCAGCCAGAGGCGGTGGAGAGGAGGAAGGGGCGGGGTGGGGGGCA  
 GAGAGCGGGCCGAGGCCGCCCTTGGTGGGGGTAGCGGGGCGAGAGCTGCCGAGCAGACCCGGCAGCCGCCCTCCTCC  
 GCCCCACCTCCAGAAGCACTCTTGCTGAGAACCGAATTATTCACCTAGTATTATTTTCATTTTTTATTACTCCCC  
 CTCCTCACTCCCCAGCCGCCCCACCCCCACGCCGGCTCGCCTCTGGTTGCATGGCAGCGCTGCCCCGGGCGCGGGG  
 GCTCAGGGCTGGCCCCAGGGAAGGGGGAGGAGGAGGAGGATCATGAAGGCCGGAGTCGCGACCGCGCCGGACGGCG  
 GGCAGCAGCCAGAGGACGAGCCGGAGCAGCCCCCGCCCCGGAGACACCCGGACGCGGAGCAGCAGTCGCCTCCGCCG  
 CCGCAGCAGCAGCTGCGGGCGCGGGCCGACCCGGAGCCGGAGGAGGAGGGCGACCCGACCCAGAGGAGGAAGAGGA  
 GGAGAAGGCGAGGCCACTCGCCCGCCGGACCTGCCCTTCTCTCGGCTCTTGCCCTCGACCGAAGGGACCTTTGAT  
 GGAACCCGAGGGGAGGGCGCCACGGATTTGCCGACTGCAGCAGGGGTGGGCTGGGGCTGAGATAATGTAAACCACTCC  
 TTTCTCCTGTTCTCTCCACACGCCCTCTCCTCTACCCCTATTCTCTGCTCCACTGCCCTCTACCCCGGTACACA  
 CACCCTTCTCTAGCCAGGATCTTTCATGCTCAGGAAGGAGGCGCCTCTGCAAGGGTTAAACGATCTTTTCTTTTCT  
 CCCATCCTTTTTCCTTCCCCAACCTCTATTTTACCTCCCTTCTCCTAATTGGCTTTCCCTCTTCGGTGTAAACCTT  
 TGGCTGCGGAGGCAAAGCACAAGCCCCTAGCCAGTTTACCTGCAACACCCCTCCCCACCCAACCTGCTCTCTTAA  
 AAGCAACTCTGGTGCTTCTGGGGTTAATTGCCCCAGTTTTCTGCCAGGAGAATTAAACTTCTCCCAATCTTCTC  
 TCCTCCCTACCTTGACTCCCCCAACCCCTACCACCTGAGAAAAACGATCTTTTCTCTCTCACACATGCAGTCCCTCA  
 ATTCTTCATTGAGCTAGTTTTCTCTAAGCCAGCTCAATCCACTCCAGATTTGATTTACAATTGTCCCCACCCCTTTT  
 ATATAAAGAAAGATTTCTCACTGCGTAGGAATTTGAGAAGAACCATAATCCTTTCTGGGGAACTTTAAACAA  
 TTCGACATTGATTTAAACAATTTCAGACAGAGGCTCTAGTGGCCCTCCACCACGCTTCTTCAATCCCTCTGCTCCTAC  
 CAGTGCTCTCAGGTCAAAGCAGAAAGGAGACACACTGAACAAAGTTGGAGGTTGGGGTGGGTGTGTGAGGGCAAGA  
 AAAACTTTTTTGTATTGGGCTTTCCAGGTGGAGTTCAGAACCAGTGACTCACACTTCTCAGTCCCTGGGAGCAATTT  
 ATTTGCTACTTGGAGGGTTGTAAGAAAAGCCAGTGAGAAAGCAGACTCCCCCACAACACAGATCCACTGTGGACC  
 CCCAAAACCTGTCTGTCCCCCTCTTTAAGACTCCAGCCACCCCTCTTGGGCTCTCTACTTCCACGGGGCACATGC  
 TGATGCCCTGTGTGGGCTGCTCTGGTGGTGGTGGTGTGCTGCTCCGGCTGGTACTGCTATGGATTGTGTGCCCA  
 GCCCCCAGATGTTGCGCCACCAGGGTCTCCTCAAGTGCCGCTGCCGATGCTCTTCAATGACCTGAAGGTTTCTT  
 ACTGCGGCGCCCTCCTCAAGCGCCCTGCCATGCACGGCGACCCCGAGCCCCCGGTTTGGCGGCCAACACACCC  
 TTCCGGCTCTGGGCGCGGGGGGTGGGCAGGCTGGAGGGGCCCCGAGAAGTGGTGGGCAGGAGCCCCCTCCTGTG  
 CCACCTCCACCCCCCTTGCCACCTTCTTCTGTGGAAGATGACTGGGGTGGCCAGCCACAGAGCCACCTGCCTCGCT  
 GCTCAGCAGTGCCCTCCTCAGATGACTTCTGTAAGGAGAAGACCGAGGATCGCTACTCACTGGGCAGCAGCTTGGACA  
 GTGGTATGAGGACCCACTCTGCCGATCTGCTTCCAGGGGCCAGAACAGGGGGAGCTGCTGAGCCCATGCCGCTGT  
 GATGGCTCGGTCAAGTGACACACCAGCCTTGCCCTCATCAAGTGGATCAGCGAGCGGGGCTGCTGGAGCTGCGAGCT  
 GTGCTACTACAGTACCACGTCAATCGCCATAAGCACAAAAATCCTCTGCAGTGGCAGGCCATCTCTGACGGTCA  
 TTGAGAAGGTTTCAAGTTGCAGCCGCCATCCTGGGCTCCCTCTTCTCATCGCCAGTATTTCTTGGCTCATCTGGTCA  
 ACTTTCAGCCCCCTCGGCAAGATGGCAGCGCCAAGACCTTCTCTTCCAGATCTGCTACGGGATGTATGGCTTCATGGA  
 CGTGGTGTGCATAGGTCTCATCATCCATGAAGGACCCTCGGTGTACCGCATCTTTAAACGGTGGCAGGCTGTCAACC  
 AGCAGTGGAAAGTGTGAATATGACAAGACAAAAGACCTGGAGGATCAAAGGCAGGAGGCAGGACCAACCCCCGG  
 ACCTCCTCATCCACCCAGGCCAATATCCCTCCTCGGAAGAGGAGACCGCAGGCACCCCTGCCCTGAGCAGGGCCC  
 TGCCAGGCTGCCGGCCACCCCTCAGGCCCTCTGTCCATCACCCTGTGCTTATACCATCCTGCACATCCTGTAGTC  
 ACTTGAGACCTCATGAACAGCGAAGTCCCCAGGCAGCAGCCGAGAGCTGGTTCATGAGAGTCACGACAGTGTGAGAG  
 CAGAGGCCCCGAAGGAAGGCCATGACCACCACTGAGGGCCCGAGCAGGTTGGGGAGGTGCACTGGCACCCCCGGAG  
 CCAACAGAGGGAGCAGGCAGAGGGTGGGGGACCTGGCGGGAGCCCTGGGGTAGTGTGAGAGCGGGAGTGAGGCTGGT  
 GCAGGAGCAGTTCTGCTATTTCCAATCAGTCAATGCCACTCTCCACAACAACAATGAAAACCAACCAACTCAACA  
 ACAAGTGCAATACAGGCTGAACCTGGCCCAACAGAAAAACCTGCCCAATGCACCTGCAGGCAAGGTACCCGAAG  
 AAGCAGAGGCTGAGGGCAGGCAAAGCCTGTGTGACTGTGGCAGTGCCGGAGGCCAAGGGGGCCAAAGAGGAAAAGCAT  
 CTGTGGTCTGCCCTGCTCTCACCTGTTTGGTTTTGTTTTCTCTGGGGCTGTGTTCTGCAGGCAGCCAGAAAAGGAG  
 GAGGCACGGGTGAGCTGGCAGGGACACACTGCCTTTGGGGCTCCTGGGCTCATTTGGATGAGCAAGATTTCGTGACA  
 AATGGCTGTGGGGATGGTGGGGTGGATGGTCAGGGAGGGATCCTCAGGGAGGGATATGCTGGTGTGAGCAGCCAGAG  
 GGAGAGTGTGTCTCCTTCCCTGAAGGAACTTCCAAATGGAACCTCCGATTTAGGTGGGCTAAAAGAGGGCTTAGGTT  
 TGGAAAAGGGTGTCTTCTGTGCCCTTGTTAATTTATTTATAGTGATTTGGTTCAAAGATGTTTACAGGACACACA  
 CACACACACACACACACACACACACACACACACACACACCCCTAGAGAAAAGTACAGATTTCCAGTGGATATTTCAAGCAC  
 AGTTCTGCTGCTGTGGCTTCAGCTTTGGAAGCTGTCAATCCCGGAGCAACTTTCCCAACTACCAACCCACCATGG  
 CCAGGACATGTGCAATGCCAGCCCTTCTTGTCTTGGCAGATGCACAGACCCAGTCCCTCAGCGTAGG

**FIGURE 72B**

GCACCCCTGACCTACGGGCTTCCAAGAGAGCAGCTGCAGTGGTTGGGAGGAGCTTGACCAGTGTGCCCCAAGGAGTG  
GAGTAGAGCCCAATCTAAGTATTCCCTTGCTGCTTGGAACCCCTCCCTGTTTGGAACCCCTCCCCAAAGAGGCAGTCAGG  
CTGATGCTCAGTGCTTTGTGCTCCCTGCTCCTTCCCGCGTAGCCAGGTGGGCCCCAAGGGTGCCCTGGCAGGGAGCACT  
ACCCCTGGACCCCTCCTGCTCGCTCTGGGGACCCCTGCCAGGGAAGGCCACTGGGTGTTACCTGCAAAGTTTCTGGT  
TGTCAGTGCACAGTGGTCGCGTCATCCATGGGTATTAAAAGGACACTGTCAAGTACTTTTTTAAACTAGTTTTTAGG  
GTTTTTTAAAACTCTCTGTTGTTGTAATATTCTCTTAAAAGCTTGAAAATAAACTTCTTCCCTACC

FIGURE 73



**FIGURE 74A**

CTGCCCCCTGGGTCTCTGCGCCTTTGCATGAGACTTTACGGTAAGCCGCTCCTCCCGCGCCCCCGCCCCAGCCCCGC  
 TCGGCGATCCCCGGCGCCGTCGCCAGGCGCTGGCCGTGGTGCTGATTCTGTGTCAGGCGCTGGCGGGCGAGCGGCGGT  
 GACGGCTGCGGCCCCGCTCCCTCTACCCGGCCGACCCGGCTCTGCCCCCGCGCCCAAGCCCCACCAAGCCCCCGC  
 CCTCCCGCCGCGGTCCAGCCCCAGGGCGCGGCCGCAACCAGCACCA**ATG**CGCCCGGTAGCCCTGCTGCTCCTGCCCTC  
 GCTGCTGGCGCTCCTGGCTCACGGACTCTCTTTAGAGGCCCAACCGTGGGGAAAGGACAAGCCCCAGGCATCGAGG  
 AGACAGATGGCGAGCTGACAGCAGCCCCACACCTGAGCAGCCAGAACGAGGCGTCCACTTTGTACAAACAGCCCC  
 ACCTTGAAGCTGCTCAACCACCACCCGCTGCTTGAGGAATTCTTACACGAGGGGCTGGAAAAGGGAGATGAGGAGCT  
 GAGGCCAGCACTGTCTTTAGCCTGACCCACCTGCACCCTTACCCCAAGTCCCCTTCCCCGCTGGCCAAACCAGG  
 ACAGCCGCCCTGTCTTTACCAGCCCCACTCCAGCCATGGCTGCGGTACCCACTCAGCCCCAGTCCAAGGAGGGACCC  
 TGGAGTCCGGATCCGGAGTCAGAGTCCCTATGCTTGAATCACAGCTCCCTACCTCCAGGGCCAGCATGGCAGT  
 GCCCCACCTAGGCCAGGGGAGATAGCCAGCACTACACCCCCAGCAGAGCCTGGACACCAACCCAAGAGGGTCTTG  
 GAGACATGGGAAGGCCGTGGGTTGCAGAGGTTGTGTCCAGGGCGCAGGGATCGGGATCCAGGGGACCATCACCTCC  
 TCCACAGCTTCAGGAGATGATGAGGAGACCACCTACCACCACCATCATCACACCACCATCACACAGTCCAGAC  
 ACCAGGCCCTTGAGCTGGAATTTCTCAGGCCAGAGGGCTCTCTGGACTCCCTACAGACCTCAGTCCCCCACTG  
 ATGTTGGCCTGGACTGCTTCTTCTACATCTCTGTCTAGGCTATGGCGTGAATCAAGGTCAAGAATATCAGC  
 CTCCGGGAAGGGGAGACAGTGAAGGCTGAGGGGGGCTGACCCACTGCCCTGGCCAACCACTGCTTCTCT  
 GCTGCGGGGCCAAGTCATCCGAGCCCCACCAAGCGGCCCTGAGGTTCCAGAGCCTCCCGCCACCGGCTGGCC  
 CTGGCACCTTCCATTTCATTACCAAGCCTATCTCTGAGCTGCCACTTCCCCGCTCGTCCAGCTTATGGAGATGTG  
 ACTGTACCCAGCCTCCACCCAGGGGGTAGTGCCCGCTTCCATTGTGCCACTGGCTACCAGCTGAAGGGCGCCAGGCA  
 TCTCACCTGTCTCAATGCCACCCAGCCCTTCTGGGATTCAAAGGAGCCCGTCTGCATCGGTGAGTGCCAGGGGTGA  
 TCCGCAATGCCACCCAGCGCCGCATCGTCTCTCCAGGCTTCCCGGGCAACTACAGCAACAACCTCACCTGTCACTGG  
 CTGCTTGAGGCTCCTGAGGGCCAGCGCTACACCTGCACCTTTGAGAAGGTTTCCCTGGCAGAGGATGATGACAGGCT  
 CATCATTCGAATGGGGACAACGTGGAGGCCCCACCAAGTGTATGATTCTATGAGGTGGAATACCTGCCCATTGAGG  
 GCCTGCTCAGCTCTGGCAAACACTTCTTTGTTGAGCTCAGTACTGACAGCAGCGGGGAGCTGCAGGCATGGCCCTG  
 CGCTATGAGGCCCTCCAGCAGGGCCATTGCTATGAGCCCTTTGTCAAATACGGTAACCTCAGCAGCAGCACACCCAC  
 CTACCCCTGTGGGTACCACTGTGGAGTTCACTGCTGACCCCTGAGCTACCCCTGGAGCAGGGCTCCATCATCGAGT  
 GTGTTGACCCCCACGACCCCCAGTGAATGAGACAGCCAGCCTGCCGAGCCGTGTGACGCGGGGAGATCACAGAC  
 TCGGCTGGCGTGGTACTCTCTCCCACTGGCCAGAGCCCTACGGTCTGTTGGCAGGATTGTATCTGGGGTGTGCATGT  
 GGAAGAGGACAAGCGCATCATGTGGACATCCGAGTGTGCGCATAGGCCCTGGTGATGTGCTTACCTTCTATGATG  
 GGGATGACCTGACGGCCCGGTTCTGGGCCAGTACTCAGGGCCCCGTAGCCACTTCAAGCTCTTTACCTCCATGGCT  
 GATGTACCATTCAGTTCCAGTCCGACCCCGGACCTCAGTGTGGGCTACCAGCAGGGCTTCGTCATCCACTTCTT  
 TGAGGTGCCCCGCAATGACACATGTCCGGAGCTGCTGAGATCCCCAATGGCTGGAAGAGCCCATCGCAGCCTGAGC  
 TAGTGCACGGCACCGTGGTCACTTACCAGTGTACCTGGCTACCAGGTAGTGGGATCCAGTGTCTCATGTGCCAG  
 TGGGACCTAACTTGGAGTGAGGACCTGCCCTCATGCCAGAGGGTGACTTCTGCCACGATCCTGGAGATGTGGAGCA  
 CAGCCGACGCCCTCATATCCAGCCCCAAGTTTCCCGTGGGGGCCACCGTGCAATATATCTGTGACCAGGGTTTTGTGC  
 TGATGGGCAGCTCCATCCTCACCTGCCATGATCGCCAGGCTGGCAGCCCCAAGTGGAGTGACCGGGCCCCCTAAATGT  
 CTCCTGGAACAGCTCAAGCCATGCCATGGTCTCAGTGCCCCCTGAGAATGGTGCCCGAAGTCTGAGAAGCAGCTACA  
 CCCAGCAGGGGCCACCATCCACTTCTCGTGTGCCCCCTGGCTATGTGCTGAAGGGCCAGGCCAGCATCAAGTGTGTGC  
 CTGGGCACCCCTCGCATTGGAGTGACCCCCCACCCTCTGTAGGGCTGCCTCTCTGGATGGTTCTACAACAGTTCGA  
 GCCTGGATGGTTGCCAAGGCACCTGCTGCCTCCAGCACCCTGGATGCTGCCACATTGCAGCTGCCATCTTCTTGCC  
 ACTGGTGGCGATGGTGTGTTGGTAGGAGGTGATACTTCTACTTCTCCAGGCTCCAGGGAAAAAGCTCCCTGCAGC  
 TGCCCCGCCCCCGCCCCCTACAACCGCATTACCATAGAGTCAGCGTTTGACAATCCAACCTACGAGACTGGA  
 TCTCTTTCCCTTTGCAAGGAGACGAGAGAATA**TGA**AGTCTCCATCTAGGTGGGGGCAGTCTAGGGAAGTCAACTCAGAC  
 TTGCACCACAGTCCAGCAGCAAGGCTCCTTGCTTCTGCTGTCCCTCCACCTCCTGTATATACCACCTAGGAGGAGA  
 TGCCACCAAGCCCTCAAGAAGTTGTGCCCTTCCCCGCTGCGATGCCACCATGGCCTATTTTCTTGGTGTCAATTGC  
 CCACTTGGGGCCCTTCATTGGGCCCATGTGAGGGGCGATCTACCTGTGGGAAGAACATAGCTGGAGCACAAGCATCA  
 ACAGCCGGCATCCTGAGCCTCCTCATGCCCTGGACCAGCCTGGAACACACTAGCAGAGCAGGAGTACCTTTCTCCAC  
 ATGACCACCATCCCGCCCTGGCATGGCAACCTGCAGCAGGATTAACCTTGACCATGGTGGGAACCTGCACAGGGTACT  
 CCTCACAGCGCCATACCAATGGCCAAAACCTCTCTCAACGGTGACCTCTGGGTAGTCTTGGCATGCCAACATCAGC  
 CTCTTGGGAGGTCTCTAGTTCTCTAAAGTTCTGGACAGTTCTGCCTCCTGCCCTGTCCCAGTGGAGGCAGTAATTCT  
 AGGAGATCCTAAGGGGTTTCAAGGGGACCCTACCCCCACCTCAGGTTGGGCTTCCCTGGGCACCTCATGCTCCACACCA  
 AAGCAGGACACGCCATTTTCCACTGACCACCCTATACCTGAGGAAAGGGAGACTTTCCCTCCGATGTTT

**FIGURE 74B**

ATTTAGCTGTTGCAAACATCTTCACCCTAATAGTCCCTCCTCCAATTCCAGCCACTTGTCAGGCTCTCCTCTTGACC  
ACTGTGTTATGGGATAAGGGGAGGGGGTGGGCATATTCTGGAGAGGAGCAGAGGTCCAAGGACCCAGGAATTTGGCA  
TGGAACAGGTGGTAGGAGAGCCCCAGGGAGACGCCCAGGAGCTGGCTGAAAGCCACTTTGTACATGTAATGTATTAT  
ATGGGGTCTGGGCTCCAGCCAGAGAACAAATCTTTATTTCTGTTGTTTCCTTATTAAAATGGTGTTTTTGGAACAAAAA

**FIGURE 75A**

**FIGURE 75B**

ACATGCACACAGACCACATAGCACACATGTGCACTGACCACACCTGTATAGACCATGCACAGTACACATACGTGCAT  
 ACACATGCCTGCATACAGGCATACACATGCACGCTTACATGTACACGTGCACAGATCACACACATGCACACACGTGT  
 AGCTCACACACAGTATACACATACACAAGTGCACAGACCACACACAGCACTAACACATGCACACACAAAGTGCATAG  
 GCCACACAGCACATGCACACAGGTGCACAGACCACACAGCACACACAAGTGCACAGAGCACACTGCACACATGCACA  
 CACACACGCGTGCATGCACACTCCTCGCACTTCCAGCCTTGGAGCCCTTCTGTCTCTGGTCTTTCTCTTTGACCCTG  
 CTGAGTGTAAAGCTGCCTGGGGAGGGGCTACAAGGAGTAATTGTGGCTTTAGGGGTCGTGGTGATGCTGGAATGTCAA  
 GCGCCGTCGTGGGGTATCCGACTGTCCGGGCTCCTGGTCCGAGTGGCAGAGCGCCAGGCAGAGCCAATCAGGGTCT  
 CGTGCTGCCCTTCCCCCCCACAGCCTGGCAGCCATCCAGAGGAGGGGCTCTACCAGATGCCAAGGTGCCCGGTGTC  
 TGTATGGGTGTCCGGTTGGGTCTGTGTTTGGTCTGCCCTGGAGGTGGCTGGGCCCTCCTGGGATGGGTGGCTCAGC  
 CTCGAATCCCAGGCCCCAGCCCAGGCAGGTGCTGCTGCCTGTTGTGGTTTCTGGCCAGCTTCTCCTTCTCCCTCT  
 GCATAAAATCACAGTCCGTGAGTCTTCCAGCTGCCACCACGGCTGGGACACGCTGGGGGAGGGCTCCTCCCATGCCT  
 CCTGCACACAGCCGTCTGAGCAGGGCAGGTGCCAACCCCCCACCAGGAGACACGCTGCCCCCTCAGCGATGCCCTTA  
 CCTTTTGGGGGGCCTCGTCTCAAGCCCCCCTTGGAGGCTGAAATCACCCAGGCAGTGTAGGGGCTTCTCCAGGGG  
 GACACCCTTTGAGCTGTGGGTCTGATCACCCCAAGTCCCGCACACGGAGGAGAGGCACAGCCAGGGCGTGTGGTTTA  
 ATGTTTGGCCCTTTCGGGGCTGGAGGTCTCAGTGTCTTAGATTCCAGACCCTGCTGCCAGAGAGACCTGCTGCCGGA  
 GAGAAGGGGAGGAGGACTCCAGCTGGGCTCGGTCCCCACAGTCAGGGACCCCATAAAGGACACCCCTTCTCTCT  
 AGAAAAGAGCTGGGCTCTCAGCTATTTCTAGTTGCTTCCAGAAGCCGAGGAGCAGAAGGAGCTGTGAGAGCTTTGCA  
 GAAACGCCCTTGTCCCCGCCCTCCTGAGCTATGAATGCCGTACAGAGCAGAGGCTGGGGCATTGGCAAGATCACAGG  
 TTGATGCTGCACAGCCCCATTGACACAAACCTCAAAGCAGACGTGAGAGGGACGGTTTCAAAAGCTTGGACCTGCC  
 GTGGAGGGTGGCCGGCAGACGTGGCGTGAGAGGGACGGCTCACGAGGCTTGGACCTGCTGTGGAGGGTGGCCAGCAG  
 ACGTGGTGTGAGAGGAACGGCTCACGAGACTTGGACCTGGTGGAGGGTGCCAGCAGACGTGGTGTGAGAGGGACGG  
 CTCACAGGGCTTGGACCGGAGAGAGATGGCTCATGAGACTTGGACCTGCCGTGGAGGGTGGCCAGCAGACGTGGTAT  
 GAGAGGGATGGCTCACGAGGCTTGGACCTGGTGGAGGGTGGCCGGCAGACGTGTGAGAGGGACGGTTACAAGGCTT  
 GGACCTGCCATGGAGGGTGGCCAGCAGACGTGGTGTGAGAGGGACAGCTCACGAGGCTTGGACCTGCCGTGGAGGGT  
 GCCCAGCAGGGGGCTGAGCTCTGAGGGGTGGGTGCTCAGTGCACGGGTGCCCCAGTGTCTCTGATCCTGTCCGGT  
 GCCTCCCCCAACCCCAACCCATGCAGAACTCCAGGTCACATGCACGTATGTCCAGGGCATGGGGGTGGCGTGAA  
 GAGGCCTGGTCAGGGCCTTTAGGGGCTGCAGGACGGAATGGCCACCTGGGGAGCCTGTGTGGCTGTGCCGGGCAGCC  
 ATCCTGCATTCCCACCCAGCGCGCAGTCTCCACCTCGGCCCCAGCAAAGCGCTAAGCAGCCGGAGAGACAGCCAGGG  
 CGGCTTCTGAAGGATGTGGGATGGTGGACTCCGGGGTTCGAGGGAATACGCAGGTTCTGTCTCCGGGAGACCTAG  
 AGAAGCTGCACACCCAGGAGCTTCCATGACCCGGGAGCATGAGTGAATGGGGGGTCCAGTTTGTGTAAGCTTTGCT  
 GTCTTGTAAGGGTGGGGGCTGACGGCCGACCCTGGGAGGAGGTGACACCGCAGGGGGAGGTTGTGGGCAACGGTGGA  
 GGAGGAGAGACGGGAGGGGACCATTGGGATGGAGGGGCTCTTCAGAGTTTAAAGGCGTTTGTGGGGTGGAGTT  
 GAGTGTGCTCTGGGCTTGGACACTTGCCGTGGTGGCCCTGGCTGGCCGAGGAGACTGGCTCTGGCCAGGGCCCCGTC  
 CTGAGAGGTCTCAGCGTCTGACTCTCGGCCAGGCGCCAGCAAGGAGGGGCGGTCCCCGGGGCTACCAGGCAGGCA  
 CGTGCACATCGCCATCGCCACACGCCAACTCCGCTGGGTTTTACAAAGTCGTTGCCTTAATGCATGTGGACAGGAA  
 CTCCCTGAGGTGCCCCATGCCCCCTGGCTGTGCCAGGTACGGACGCCCTGGACCTTGCGAACAGGTGGGGCGGGCG  
 AGGGGCCCCAAGGGACGGGCTCCAGAGACACGCGCAGGGCAGGAGGGTCTCACGAGGGGTCTCGCACTGAGGCGCC  
 CAGAGCTGGTGGTCCCGCTGGACGCCATCCCTCTGCCCGGATCCACACGGGCCACGTGTGCCCGCCATGCCCGCGC  
 CCCACGCCATTGCACTCTTCCATCCTCTGGCCGTGACGGTGGCTGCAGCTTCCCCATTTGCGCCGTGTCCTCTGGCT  
 GTCTGCACTTTTGTTCATGCTCCAAAGAACATTTTATAATGCCTTACGTACCGACGTACACTTCTGACCATTTTGT  
 TGTGTCCTTGTGCCGTAGTGACCAGGCCTTTTTTGGTGGATGTGTTACCCCGCACACTTCAATCTCAACTTTGTGC  
 ACCGTCCATTTTCTAGGGATAGACGCCAGGGAATGAACTCTAGTTTTCTAACAGATTAGCTGAGATATTAACCTTAC  
 TCACACGGACAGGTTGATGCCAGAGCCGTAAGAATGCCCAGTGCGGGTTTGCGGGGGACTTCGGGTGTGGGGTCT  
 GCGGCCGCGATGGCCGTGGAAGGTTCTGGGGATCCCTGCTGCCACGGGGACGAGTTTCGGACGCCAGGTGGACCTGTG  
 CACTCAGTAAAACGCAGTGATTCAAAAA

**FIGURE 76**

GGCACGAGGCAAGTCCGGATGAAGAATTAAGAGAAAAAAGTGAATATGGTTTTTGCTCACAGAATGGATAACAGCA  
AGCCACATTTGATTATTCTACACTTCTGGTGCCCCCTCCAAAACCGCAGCTGCACTGAAACAGCCACACCTCTGCCA  
AGCCAATACCTGATGGAATTAAGTGAGGAGCACAGTTGGATGAGCAACCAAACAGACCTTCACTATGTGCTGAAACC  
CGGGGAAGTGGCCACAGCCAGCATCTTCTTTGGGATTCTGTGGTTGTTTTCTATCTTCGGCAATTCCTGGTTTGTT  
TGGTCATCCATAGGAGTAGGAGGACTCAGTCTACCACCAACTACTTTGTGGTCTCCATGGCATGTGCTGACCTTCTC  
ATCAGCGTTGCCAGCACGCCTTTCGTCCTGCTCCAGTTCACCACTGGAAGGTGGACGCTGGGTAGTGCAACGTGCAA  
GGTTGTGCGATATTTTCAATATCTCACTCCAGGTGTCCAGATCTACGTTCTCCTCTCCATCTGCATAGACCGGTTCT  
ACACCATCGTCTATCCTCTGAGCTTCAAGGTGTCCAGAGAAAAAGCCAAGAAAATGATTGCGGCATCGTGGATCTTT  
GATGCAGGCTTTGTGACCCCTGTGCTCTTTTTCTATGGCTCCAACCTGGGACAGTCATTGTAACATTTTCTCCCTC  
CTCTTGGGAAGGCACTGCCTACACTGTCTATCCACTTCTTGGTGGGCTTTGTGATTCCATCTGTCTCATAATTTTAT  
TTTACCAAAGGTCATAAAATATATTTGGAGAATAGGCACAGATGGCCGAACGGTGAGGAGGACAATGAACATTGTC  
CCTCGGACAAAAGTGAAACTATCAAGATGTTCTCATTTTAAATCTGTTGTTTTTGCTCTCTGGCTGCCTTTTCA  
TG TAGCTCAGCTATGGCACCCCATGAACAAGACTATAAGAAAAGTTCCCTTGTTTTTCACAGCTATCACATGGATAT  
CCTTTAGTTCTTCAGCCTCTAAACCTACTCTGTATTCAATTTATAATGCCAATTTTCGGAGAGGGATGAAAGAGACT  
TTTTGCATGTCTCTATGAAATGTTACCGAAGCAATGCCTATACTATTACAACAAGTTCAAGGATGGCCAAAAA  
CTACGTTGGCATTTCAGAAATCCCTTCCATGGCCAAAACCTATTACCAAAGACTCGATCTATGACTCATTGACAGAG  
AAGCCAAGGAAAAAAGCTTGCTTGGCCATTAACTCAAATCCACCAAATACTTTTGTCTTAAGTTCTCATTCTTTCA  
ATTGTTATGCACCAGAGATTAAAAAGCTTAACTATAAAAAACAGAAGCTATTTACATATTTGTTTTCACTCAACTTT  
CCAAGGGAAATGTTTTATTTGTAAATGCATTCATTTGTTTACTGT

**FIGURE 77**

GCCATGGCCGTCGCGCCCGGCCTGTGGCCAGCGCTCCTGGGCATAGTCCTCGCCGCTTGGCCTCGCGGCTCGGGTGC  
 CCAGCAGAGTGCCACCGTGGCCAACCCAGTGCTGGTGCCAACCCGACCTGCTTCCCCACTTCTTGGTGGAGCCCG  
 AGGATGTGTACATCGTCAAGAACAAGCCAGTGCTGCTTGTGTGCAAGGCCGTGCCCGCCACGCAGATCTTCTTCAAG  
 TGCAACGGGGAGTGGGTGCGCCAGGTGGACCACGTGATCGAGCGCAGCACAGACGGGAGCAGTGGGCTGCCACCAT  
 GGAGGTCCGCATTAAATGTCTCAAGGCAGCAGGTGAGAAAGGTGTTTCGGGCTGGAGGAATACTGGTGCCAGTGCGTGG  
 CATGGAGCTCCTCGGGCACCACCAAGAGTCAGAAGGCCATACATCCGCATAGCCTATTTGCGCAAGAATTTCGAGCAG  
 GAGCCGCTGGCCAAGGAGGTGTCCCTGGAGCAGGGCATCGTGCTGCCCTGCCGTCCACCGGAGGGCATCCCTCCAGC  
 CGAGGTGGAGTGGCTCCGGAACGAGGACCTGGTGGACCCGTCCTGGACCCCAATGTATACATCACGCGGGAGCACA  
 GCCTGGTGGTGCGACAGGCCCGCCTTGTGACACGGCCAACTACACCTGCGTGGCCAAGAATCGTGGCAGCTGCG  
 CGCAGCGCCTCCGCTGCTGTATCGTCTACGTGGACGGCAGCTGGAGCCCGTGGAGCAAGTGGTGGGCTGTGGGCT  
 GGACTGCACCCACTGGCGGAGCCGTGAGTGCTGTGACCCAGCACCCCGCAACGGAGGGGAGGAGTGCCAGGGCACTG  
 ACCTGGACACCCGCAACTGTACAGTGACCTCTGTGTACACACTGCTTCTGGCCCTGAGGACGTGGCCCTCTATGTG  
 GGCCTCATCGCGTGGCCGTCTGCCTGGTCCGTGCTGCTTGTCTCATCTCGTTTATTGCCGGAAGAGGAGGG  
 GCTGGACTCAGATGTGGCTGACTCGTCCATTCTCACCTCAGGCTTCCAGCCCGTCAGCATCAAGCCCAGCAAAGCAG  
 ACAACCCCCATCTGCTCACCATCCAGCCGACCTCAGCACCACCACCACCTACCAGGGCAGTCTCTGTCCCCGG  
 CAGGATGGGCCCCAGCCCCAAGTTCAGCTCACCATGGGCACCTGCTAGCCCCCTGGGAGCAGCTGAGCCCTGAGCAGT  
 GCACCACAGCTCTCCACCTCTGAGGCCGAGGAGTTCGTCTCCCGCCTCTCCACCCAGAATACTTCCGCTCCCTGC  
 CCGAGGCACCAGCAACATGACCTATGGGACCTTCAACTTCTCGGGGGCCGGCTGATGATCCCTAATACAGGAATC  
 AGCCTCCTCATCCCCCAGATGCCATACCCCGAGGGAGATCTATGAGATCTACCTCACGCTGCACAAGCCGGAAGA  
 CGTGAGGTTGCCCTAGCTGGCTGTGACCCCTGCTGAGTCCCATCGTTAGCTGTGGACCCCTGGCGTCCCTGCTCA  
 CCCGGCCAGTCATCCTGGCTATGGACCCTGTGGGGAGCCAGCCCTGACAGCTGGAGCCTGCGCCTCAAAAAGCAG  
 TCGTGCGAGGGCAGCTGGGAGGATGTGCTGCACCTGGGCGAGGAGGCGCCCTCCACCTCTACTACTGCCAGCTGGA  
 GGCCAGTGCTGTACGTCTTACCAGCAGCTGGGCGCTTTGCCCTGGTGGGAGAGGCCCTCAGCGTGGCTGCCG  
 CCAAGCGCCTCAAGCTGCTTCTGTTTGCGCCGGTGGCCTGCACCTCCCTCGAGTACAACATCCGGGTCTACTGCCTG  
 CATGACACCCACGATGCACTCAAGGAGGTGGTGCAGCTGGAGAAGCAGCTGGGGGGACAGCTGATCCAGGAGCCACG  
 GGTCCCTGCACTTCAAGGACAGTTACCACAACCTGCGCCTATCCATCCACGATGTGCCAGCTCCCTGTGGAAGAGTA  
 AGCTCCTTGTGCTAGCTACCAGGAGATCCCCCTTTTATCACATCTGGAATGGCACGCGAGCGGTACTTGCACTGCACCTT  
 ACCCTGGAGCGTGTGAGCCCCAGCACTAGTGACCTGGCCTGCAAGCTGTGGGTGTGGCAGGTGGAGGGCGACGGGCA  
 GAGCTTCAGCATCAACTTCAACATCACCAAGGACACAAGGTTTGTGCTGAGCTGCTGGCTCTGGAGAGTGAAGCGGGG  
 TCCCAGCCCTGGTGGGCCCCAGTGCCCTTCAAGATCCCCCTTCTCATTCGGCAGAGAATAATTTCCAGCCTGGACCCA  
 CCCTGTAGGCGGGGTGCCGACTGGCGGACTCTGGCCCAGAACTCCACCTGGACAGCCATCTCAGCTTCTTTGCCTC  
 CAAGCCCAGCCCCACAGCCATGATCCTCAACCTGTGGGAGGCGCGCACTTCCCCAACGGCAACCTCAGCCAGCTGG  
 CTGCAGCAGTGGCTGGACTGGGCCAGCCAGACGCTGGCCTCTTACAGTGTGCGAGGCTGAGTGCTTGAGGCCGGCCA  
 GGCCCGACACCTACACTCTCACCAGCTTTGGCACCCACCAAGGACAGGCAGAGCCGGACAGGGGCCCTTCCCCACA  
 CCGGGGAGAGCTGCTCGGACAGGCCCTCCCGGCCGAAGCTGTCCCTTAATGCTGGTCCCTCAGACCTGCCCGAA  
 CTCCCACCTCTCCATGGCCTGCCCTAGCCAGGCTGGCACTGCCACTCACACTCGGCCCCAGGGCCCAGGAGGGACAGT  
 GCCTGGAGCCTGGGCCAGGCCAGCCATCTGTGTGTGTATGTGCGTGTGATGCTACCTCTCCTCCCGTCCCTCT  
 CCAGGGGCCCCGCATACACACGGCCATGCACGCACACACTGGGCCTGGGCCAGGGCCCCAGAGCTCCTGCCTGAGCT  
 GGACCTTATGCAAAACATTTCTGTGCCTGCTGGGTAGGGGCACGCTCTGAGGGGCCCTGCTCCAAGCCTGCAGGACCGA  
 GGGCCACAGCCGACAGGGGGTAGCCCCCTGGATTAGGCACACGACCACCACAGAGCAGTGCACGCTACGCTCG  
 TGTGCTCATCTCACACACACCCCCCTCCCGGGTCACGCAGACACCCCCCAACCACACACATCTCATGCCGTACACCT  
 GAGGCTGCTCAGTCTCACGCCAGTGTGGTGCACATTTGCCTCTCACATGCTGCCCTCTCCACCCACCCAGGGAC  
 ACCCCACGCTCCTCCTGCCCTGCCCTCCCCAGCCTTGAGGTGCCCTGCCCGGCGGGGCTGTGAATATGCAA  
 TGGGAGTCCCAGGCTGTACAGTGGTGAAGTGTGTGTGGCGTGGCGTGGCGTCCCCAGGGCTGGCTGGTGGCCAC  
 GCGGGGCTGTATGTGAAGCTCGTGTCTGACTTTGTCTTAAGTGCATTACGCACTTACTCTGGCCTTATGTAC  
 ACAGCCTTGCCCGGCCGCGGGGCACATAGGGGTTTTATCGGGCGTGAATGTAAATAAATTATATATATATTGCT  
 AAAAAAAAAAAAAAAAAA

**FIGURE 78A**

TAAGGTAATTCGTATGCAAGAAGCTACACGTAATTAAATGTGCAGGATGAAAAGATGGCACAGGCACTGTTGGTACC  
 CCCAGGACCTGAAAGCTTCCGCCCTTTTACTAGAGAATCTCTTGCTGCTATCGAAAAACGTGCTGCAGAAGAGAAAAG  
 CCAAGAAGCCCCAAAAGGAACAAGATAATGATGATGAGAACAACCAAAGCCAAATAGTGACTTGGAAAGCTGGAAAAG  
 AACCTTCCATTTATTTATGGAGACATTCCCTCCAGAGATGGTGTGAGAGCCCCCTGGAGGACCTGGATCCCTACTATAT  
 CAATAAGAAAACCTTTTATAGTAATGAATAAAGGAAAGGCAATTTTCCGATTTCAGTGCCACCTCTGCCTGTATATTT  
 TAACTCCACTAAACCTGTTAGGAAAATTGCTATCAAGATTTTGGTACATTCTTTATTCAGCATGCTTATCATGTGC  
 ACTATTTTGACCAACTGTGTATTTATGACCTTGAGCAACCCCTCCTGACTGGACAAAGAATGTAGAGTACACATTAC  
 TGGAACTCTATACCTTTGAGTCACCTTATAAAAACTTTGGTAAGAGGGTTTTGCTTAGAAGATTTTACGTTTCTTCGTG  
 ATCCATGGAACCTGGCTGGATTTCAGTGTCAATTGTGATGGCGTATGTAACAGAATTTGTAAGCCTAGGCAATGTTTCA  
 GCCCTTCGAACTTTTCAGAGTCTTGAGAGCTCTGAAAACATATTTCTGTAATTCCAGGTTTAAAGACCATTGTGGGGGC  
 CCTGATCCAGTCGGTAAAGAAGCTTTCTGATGTGATGATCCTGACTGTGTTCTGTCTGAGCGTGTTTGTCTCTCATTG  
 GGCTGCAGCTGTTTCATGGGCAATCTGAGGAATAAATGTTTGCAGTGGCCCCCAAGCGATTCTGCTTTTGAACCAAC  
 ACCACTTCTACTTTAATGGCACAATGGATTCAAATGGGACATTTGTTAATGTACAATGAGCACATTTAACTGGAA  
 GGATAACATTGGAGATGACAGTCACCTTTATGTTTTGGATGGGCAAAAAGACCCTTTACTCTGTGGAAATGGTTCAG  
 ATGCAGGCCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTCGAAACCCCACTATGGCTACACAAGCTTTGAC  
 ACCTTTAGCTGGGCTTTCTGTCTCTATTTTCGACTCATGACTCAAGACTACTGGGAAAATCTTTACCAGTTGACATT  
 ACGTGTCTGTGGGAAAACATACAGATATTTTTGTCTGGTCATTTTCTTGGGCTCATTTTATTTGGTGAATTTGA  
 TCCTGGCTGTGGTGGCCATGGCCTATGAGGAGCAGAATCAGGCCACCTTGAAGAAGCAGAACAAAAAGAGGCCGAA  
 TTTTCAGCAGATGCTCGAACAGCTTAAAAAGCAACAGGAAGAAGCTCAGGCAGTTGCGGCAGCATCAGCTGCTCAAG  
 AGATTTTCAGTGAATAGGTGGGTTAGGAGAGCTGTTGGAAAGTTCTTCAGAAGCATCAAAGTTGAGTTCCAAAAGTG  
 CTAAGAAATGGAGGAACCGAAGGAAGAAAAGAAGACAGAGAGAGCACCTTGAAGGAAACACAAAGGAGAGAGAGAC  
 AGCTTTCCCAAATCCGAATCTGAAGACAGCGTCAAAGAAGCAGCTTCCTTTTCTCCATGGATGGAACAGAGTAC  
 CAGTGACAAAAAATCTGCTCCCTCATCAGTCTCTCTTGAGTATCCGTGGCTCCCTGTTTTCCCAAGACGCAATA  
 GCAAAACAGCATTTTTCAGTTTCAGAGGTGGGCAAAAGGATGTTGGATCTGAAAATGACTTTGCTGATGATGAACAC  
 AGCACATTTGAAGACAGCGAAACGAGGAGAGACTCACTGTTTGAGCCGCACAGACATGGAGAGCGACGCAACAGTAA  
 CGGCACCACCACAGAAACGGAGGTGAGAAAGAGAAGGTTAAGTTCTTACCAGATTTCAATGGAGATGCTGGAGGATT  
 CTTCTGGAAGGCAAAAGAGCCGTGAGCATAGCCAGCATTTCTGACCAACACAATGGAAGAATCTGAGACAG  
 AAATGTCCGCCATGCTGGTATAGATTTGCCAATGTGTTCTTGATCTGGGACTGCTGTGATGCATGGTTAAAAGTAAA  
 ACATCTGTGAATTTAATTGTTATGGATCCATTTGTTGATCTTGCCATCACTATTTGCATTGTCTTAAATACCTCT  
 TTATGGCCATGGAGCACTACCCCATGACTGAGCAATTCAGTAGTGTGTTGACTGTAGGAAACCTGGTCTTTACTGGG  
 ATTTTCACAGCAGAAATGGTCTCAAGATCATTGCCATGGATCCTTATTACTATTTCCAAGAAGGCTGGAATATCTT  
 TGAATGGAATTTATGTCAGCCTCAGTTTAAATGGAGCTTGGTCTGTCAAATGTGGAGGATTGCTGTACTGCGATCAT  
 TCAGACTGCTTAGAGTTTTCAAGTTGGCAAAATCCTGGCCACACTAAATATGCTAATTAAGATCATTGGCAATTCT  
 GTGGGGGCTCTAGGAAACCTCACCTTGGTGTGGCCATCATCGTCTTCATTTTTGCTGTGGTGGCATGCAGCTCTT  
 TGGTAAGAGCTACAAAGAATGTGTCTGCAAGATCAATGATGACTGTACGCTCCACGGTGGCACATGAACGACTTCT  
 TCCACTCCTTCTGATTGTGTTCCGCGTGCTGTGTGGAGAGTGGATAGAGACCATGTGGGACTGTATGGAGGTGCGT  
 GGCCAAACCATGTGCCTTATTGTTTTCATGTTGGTCATGGTCATTGGAAACCTTGTGGTTCTGAACCTCTTCTGGC  
 CTTATTGTTGAGTTTCATTTAGCTCAGACAACCTTGCTGCTACTGATGATGACAATGAAATGAATAATCTGCAGATTG  
 CAGTAGGAAGAATGCAAAAGGGAATTGATTATGTGAAAAATAAGATGCGGGAGTGTTTCCAAAAAGCCTTTTTTAGA  
 AAGCCAAAAGTTATAGAAATCCATGAAGGCAATAAGATAGACAGCTGCATGTCCAATAATACTGGAATTGAAATAAG  
 CAAAGCGCTTAATTATCTTAGAGATGGGAATGGAACCAACAGTGGTGTAGGTACTGGAAGCAGTGTTGAAAAATACG  
 TAATCGATGAAAATGATTATATGTCATTATAAACAACCCAGCCTCACCGTCACAGTGCCAATTGCTGTTGGAGAG  
 TCTGACTTTGAAAACCTTAAATACTGAAGAGTTTCAGCAGTGAGTCAGAACTAGAAGAAAAGCAAAGAGAAAATTAATGC  
 AACCAGCTCATCTGAAGGAAGCACAGTTGATGTTGTTCTACCCCGAGAAGGTGAACAAGCTGAAACTGAACCCGAAG  
 AAGACCTTAAACCGGAAGCTTGTCTTACTGAAGGATGTATTAAGTTTCCATTCTGTCAAGTAAGTACAGAAGAA  
 GGCAAAGGGAAGATCTGGTGGAAATCTTCGAAAAACCTGCTACAGTATGTTGAGCACAACTGGTTTGGAGCTTTTCAT  
 TGTGTTTCATGATCCTTCTCAGTAGTGGTGCATTGGCCTTTGAAGATATATACATTGAACAGCGAAAGACTATCAAAA  
 CCATGCTAGAATATGCTGACAAAGTCTTTACCTATATATTCATTCTGAAATGCTTCTCAAATGGGTTGCTTATGGA  
 TTTCAAACATATTTCACTAATGCCTGGTGGCGGCTAGATTTCTTGATCGTTGATGTTTCTTGGTTAGCCTGGTAGC  
 CAATGCTCTTGGCTACTCAGAACTCGGTGCCATCAAATCATTACGGACATTAAGAGCTTTAAGACCTCTAAGAGCCT  
 TATCCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTTGTGGAGCAATTCCTCTATCATGAATGTGCTGTTG  
 GTCTGTCTCATCTTCTGGTTGATCTTTAGCATCATGGGTGTGAATTTGTTTGGTGGCAAGTTCTACCAC

**FIGURE 78B**

TGTGTTAACATGACAACGGGTAACATGTTTGACATTAGTGATGTTAACAATTTGAGTGACTGTCAGGCTCTTGGCAA  
GCAAGCTCGGTGGAAAAACGTGAAAGTAACTTTGATAATGTTGGCGCTGGCTATCTTGCACTGCTTCAAGTGGTAAGTG



**FIGURE 79A**

AGCGAAGCGGAGGCATAAGCAGAGAGGATTCTGGAAAGGTCTCTTTGTTTTCTTATCCACAGAGAAAGAAAGAAAA  
 AAATTGTAACATAATTTGTAAACCTCTGTGGTCAAAAAAAAAAAAAAAAAAGCTGAACAGCTGCCAGAGGAAGAC  
 ACGTTATACCTAACCATCTTGGATGCTGGGCTTTGTTATGCTGTAATTCATAAGGCTCTGTTTTATCAGAGATTAT  
 GGAGCAAGAAAACTGAAGCCAAGCCACATCAAGGTTTGACAGGGATGAGATACCTGTCAAGGATTCATAGTAGAGTG  
 GCTTACTGGGAAAGGAGCAAGAATCTCTTCTAGGGATATTGTAAGAATAAATGAGATAATTCACAGAAGGGACCTG  
 GAGCTTTTCCGGAAGGAGGTGCTGTGACTATCTAAGGTAATTCGTATGCAAGAAGCTACACGTAATTAATGTGCAG  
 GATGAAAAGATGCGCACAGGCACTGTTGGTACCCAGGACCTGAAAGCTTCCGCCCTTTTACTAGAGAATCTCTTGC  
 TGCTATCGAAAAACGTGCTGCAGAAGAGAAAGCCAAGAAGCCCAAAAGGAACAAGATAATGATGATGAGAACAAC  
 CAAAGCCAAATAGTGACTTGAAGCTGGAAAGAACCTTCCATTTATTTATGGAGACATTCCTCCAGAGATGGTGTCA  
 GAGCCCCGAGGACCTGGATCCCTACTATATCAATAAGAAAACTTTTATAGTAATGAATAAAGGAAAGGCAATTTT  
 CCGATTCCAGTGGCCACCTCTGCCTTGATATTTTAACTCCACTAAACCTGTTAGGAAAATTGCTATCAAGATTTTGG  
 TACATTTCTTTATTCAGCATGCTTATCATGTGCACTATTTTGACCAACTGTGATTTTATGACCTTGAGCAACCCCTCCT  
 GACTGGACAAAGAAATGTAGAGTACACATTCACCTGGAATCTATACCTTTGAGTCACTTATAAAAAATCTTGGCAAGAGG  
 GTTTTGCTTAGAAGATTTTACGTTTCTTCGTGATCCATGGAAGTGGCTGGATTTTCACTGTGATGATGATGATGATG  
 TGACAGAGTTTGTGGACCTGGGCAATGTCTCAGCGTTGAGAACATTCAGAGTCTCCGAGCACTGAAAACAATTTCA  
 GTCATTTCCAGGTTTAAAGACCATTGTGGGGGCCCTGATCCAGTCGGTAAAGAAGCTTTCTGATGTGATGATGATGATG  
 TGTGTTCTGTCTGAGCGTGTGCTCTCATTGGGCTGCAGCTGTTTATGGGCAATCTGAGGAATAAATGTTTGCAGT  
 GGCCCCAAGCGATTCTGCTTTTGAACCAACACCCTTCTACTTTAATGGCACAATGGATTCAAATGGGACATTT  
 GTTAATGTAACAATGAGCACATTTAACTGGAAGGATTACATTGGAGATGACAGTCACTTTTATGTTTTGGATGGGCA  
 AAAAGACCCCTTACTCTGTGGAAATGGCTCAGATGCAGGCGCAGTGTCCAGAAGGATACATCTGTGTGAAGGCTGGTC  
 GAAACCCCAACTATGGCTACACAAGCTTTGACACCTTTAGCTGGGCTTCTGTCTCTATTTTCGACTACTGACTCAA  
 GACTATTGGGAAAATCTTTACCAGTTGACATTACGTGCTGCTGGGAAAACATACATGATATTTTTTGTCTCTGGTCAT  
 TTTCTTGGGCTCATTTTATTTGGTGAATTTGATCCTGGCTGTGGTGGCCATGGCCTATGAGGAGCAGAATCAGGCCA  
 CCTTGGAAAGAGCAGAACAAAAAGAGCCGAATTTTCAAGCAGATGCTCGAACAGCTTAAAAAGCAACAGGAAGAAGCT  
 CAGGCAGTTGCGGCAGCATCAGCTGCTTCAAGAGATTTTCACTGGAGTAGGTGGGTTAGGAGAGCTGTTGGAAGTTC  
 TTCAGAAGCATCAAAGTTGAGTTCCAAAGGTGCTAAAGAATTGGAGAACCCGAGGAAGAAAGAACAGAGAGAGAGC  
 ACCTTGAAGGAAACAAACAAAGGAGAGAGAGACAGCTTTCCCAATCCGAATCTGAAGACAGCGTCAAAGAGAGAGC  
 TTCCTTTTCTCCATGGATGGAAACAGACTGACCAGTGACAAAAAATTTCTGCTCCCCTCATCAGTCTCTCTGAGTAT  
 CCGTGGCTCCCTGTTTTCCCAAGACGCAATAGCAAAACAAGCATTTTCACTTTCAGAGGTGCGGCAAGGATGTTG  
 GATCTGAAAATGACTTTGCTGATGATGAACACAGCACATTTGAAGACAGCGAAAGCAGGAGAGACTCACTGTTTGTG  
 CCGCACAGACATGGAGAGCGACGCAACAGTAACGGCACCACCATGAAACGGAAGTCAGAAAGAGAAGGTTAAGCTC  
 TTACCAGATTTCAATGGAGATGCTGGAGGATTCTCTGAGGCAAGGAAAGAGCCGTGAGCATGAGCAGCATTTGACCA  
 ACACAATGGAAGAATCTGAAGAATCTAGACAGAAATGTCCGCCATGCTGGTATAGATTTGCCAATGTGTTCTTGATC  
 TGGGACTGCTGTGATGCATGGTTAAAGTAAACATCTTGTGAATTTAATTGTTATGGATCCATTTGTTGATCTTGC  
 CATCACTATTTGCATTGTCTTAAATACCCCTCTTTATGGCCATGGAGCACTACCCCATGACTGAGCAATTCAGTAGTG  
 TGTGACTGTAGGAAACCTGGTCTTTACTGGGATTTTACAGCAGAAATGGTCTCAAGATCATTGCCATGGATCCT  
 TATTACTATTTCCAAGAAGGCTGGAATATCTTTGATGGAATTTATGTGAGCCTCAGTTTAAATGGAGCTTGGTCTGTC  
 AAATGTGGAGGGATTGTCTGTACTGCGATCATTACAGACTGCTTAGAGTTTCAAGTTGGCAAAATCCTGGCCACAC  
 TAAATATGCTAATTAAGATCATTGGCAATCTGTGGGGCTCTAGGAAACCTCACCTTGGTGTGGCCATCATCGTC  
 TTCATTTTTGCTGTGGTGGCATGCAGCTCTTGGTAAGAGCTACAAAGAATGTGTCTGCAAGATCAATGATGACTG  
 TACGCTCCACGGTGGCACATGAACGACTTCTTCCACTCCTTCTGATTGTGTTCCGCGTGTGTGTGGAGAGTGG  
 TAGAGACATGTGGGACTGTATGGAGTGCCTGGCCAAACCATGTGCCTTATTGTTTTCATGTTGGTCACTGGTCACT  
 GGAACCTTGTGGTTCTGAACCTCTTTCTGGCCTTATTATTGAGTTTCAATTTAGCTCAGACAACTTGTCTACTGA  
 TGATGACAAATGAAATGAATAATCTGCAGATTGCAGTAGGAAGAATGCAAAAGGGAATTGATTATGTGAAAAATAAGA  
 TGCGGGAGTGTTCAAAAAGCCTTTTTTAGAAAGCCAAAGTTATAGAAATCCATGAAGGCAATAAGATAGACAGC  
 TGCATGTCCAATAATACTGGAATTGAAATAAGCAAGAGCTTAATTATCTTAGAGATGGGAATGGAACCACAGTGG  
 TGTAGGTACTGGAAGCAGTGTGAAAAATACGTAATCGATGAAATGATTATATGTCATTATAAACAACCCAGCC  
 TCACCGTCACAGTGCCAATTGCTGTTGGAGAGTCTGACTTTGAAAACCTTAAATACTGAAGAGTTCCAGCAGTGAGTCA  
 GAAGTGAAGAAAGCAAGAGAAATTAATGCAACCAGCTCATCTGAAGGAAGCACAGTTGATGTTGTTCTACCCCG  
 AGAAGGTGAACAAGCTGAACTGAACCCGAAGAAGACTTTAAACCGGAAGCTTGTTTTACTGAAGGTTGATTAAAA  
 AGTTTCCATTCTGTCAAGTAAGTACAGAAGAAGGCAAGGGAGATCTGGTGGAAATCTTCGAAAACCTGCTACAGT  
 ATTGTTGAGCACAACCTGGTTTGAAGCTTTTCAATGTGTTTATGATCCTTCTCAGTAGTGGTGCATTGGCCTTTGAAGA  
 TATATACATTGAACAGCGAAAGACTATCAAAACCATCTAGAAATATGCTGACAAAGTCTTACCTATATATTTCATT  
 TGGAAATGCTTCTCAAAATGGGTTGCTTATGGATTTCACACATATTTTCACTAATGCCTGGTGGTCTATATTCTTG  
 ATCGTTGATGTTTCTTTGGTTAGCCTGGTAGCCAATGCTCTTGGCTACTCAGAACTCGGTGCCATCAAATCATTACG  
 GACATTAGAGCTTTAAGACCTCTAAGAGCCTTATCCCGGTTTGAAGGCATGAGGGTGGTTGTGAATGCTCTTGTG  
 GAGCAATTCCTCTATCATGAATGTGCTGTTGGTCTGTCTCATCTTCTGGTTGATCTTTAGCATCATGGGTGTGAAT  
 TTGTTTGGTGGCAAGTTCTACCACTGTGTTAATCATGACAACGGGTAAACATGTTTGACATTAGTGATGTTAACAATTT  
 GAGTACTGTCAAGCTCTTGGCAAGCAAGCTCGGTGGAAACCTGAAAGTAAACCTTTGATAATGTTGGCCTGGCT  
 ATCTTGCACCTGCTTCAAGTGGCCACATTTAAAGGCTGGATGGATATTATGTATGCAGCTGTTGATTACAGAGATGTT  
 AAACCTCAGCCTGTATATGAAGAAAATCTGTACATGATTTTATCTTTTGTATCTTTTATCATCTTTGGGTCACTCTT  
 CACTCTGAATCTATTCAATGGTGTGATCATAGATAACTTCAACCAGCAGAAAAAGAGTTTGGAGGTCAAGACATCT  
 TTATGACAGAGGAACAGAAAAATATTACAATGCAATGAAGAACTTGGATCCAAGAAACCTCAGAAACCCATACCT

**FIGURE 79B**

CGCCCAGCAAACAAATTCCAAGGAATGGTCTTTGATTTTGTAAACCAGACAAGTCTTTGATATCAGCATCATGATCCT  
CATCTGCCTCAACATGGTCACCATGATGGTGGAAACGGATGACCAGGGCAAATACATGACCCTAGTTTTGTCCCGGA  
TCAACCTAGTGTTTATTGTTCTGTTCACTGGAGAATTTGTGCTGAAGCTCGTTTCCCTCAGACACTACTACTTCACT  
ATAGGCTGGAACATCTTTGACTTTGTGGTGGTGATTCTCTCCATTGTAGGTATGTTTCTGGCTGAGATGATAGAAAA  
GTATTCTGTGTCCCTACCTTGTTCGAGTGATCCGTCTTGCCAGGATTGGCCGAATCCTACGTCTGATCAAAGGAG  
CAAAGGGGATCCGCACGCTGCTCTTTGCTTTGATGATGTCCCTTCTGCGTTGTTAACATCGGCCCTCTGCTCTTC  
CTGGTCATGTTTATCTATGCCATCTTTGGGATGTCAAACCTTTGCCTATGTTAAAAAGGAAGCTGGAATTGATGACAT  
GTTCAACTTTGAGACCTTTGGCAACAGCATGATCTGCTTGTTCCAAATTACAACCTCTGCTGGCTGGGATGGATTGC  
TAGCACCTATTCTTAATAGTGCACCACCCGACTGTGACCCTGACACAATTCACCCTGGCAGCTCAGTTAAGGGAGAC  
CGTGGGGACCCATCTGTTGGGATTTTCTTTTTTGTGCTAGTTACATCATATCCTTCCCTGGTTGTGGTGAACATGTA  
CATCGCGGTCTCCTGGAGAATTCAGTGTTGCTACTGAAGAAAGTGCAGAGCCCCCTGAGTGAGGATGACTTTGAGA  
TGTTCTATGAGGTTTGGGAAAAGTTTGATCCCGATGCGACCCAGTTTATAGAGTTCTCTAACTCTCTGATTTTGCA  
GCTGCCCTGGATCCTCCTCTTCTCATAGCAAAACCAACAAAGTCCAGCTTATTGCCATGGATCTGCCATGGTCAG  
TGGTGACCGGATCCACTGTCTTGATATTTTATTTGCCTTTACAAAGCGTGTGTTGTGTGAGAGTGGAGAGATGGATG  
CCCTTCGAATACAGATGGAAGACAGGTTTATGGCATCAAACCCCTCCAAAGTCTCTTATGAGCCTATTACAACCACT  
TTGAAACGTAAACAGAGGAGGTGTCTGCCGTATCATTCAGCGTAATTTTCAGATGTTATCTTTTAAAGCAAAGGTT  
AAAAATATATCAAGTAACATAACAAAGAGGCAATTAAGGGAGGATTGACTTACCTATAAAACAAGACATGATTA  
TTGACAACTAAATGGGAATCCACTCCAGAAAAACAGATGGGAGTTCCCTCTACCACCTCTCTCCTTCCCTATGAT  
AGTGTAAACAAACAGACAAGGAAAAGTTTGAGAAAGACAAACCAGAAAAAGAAAGCAAAGGAAAAGAGGTGAGAGA  
AAATCAAAGTAAAGAAAGAAACAAAGAATTATCTTTGTGATCAATTGTTTACAGCCTATGAAGGTAAAGTATATGTGT  
CAACTGGACTTCAAGAGGAGGTCCATGCCAACTGACTGTTTTAACAAATACTCATAGTCAGTGCCTATACAAGACA  
GTGAAGTGACCTCTCTGTCACTGCAACTCTGTGAAGCAGGGTATCAACGTTGACAAGAGGTGTCTGTTTTATTACC  
AGCTGACACTGCTGAGGAGAAACCAATGGCTACCTAGACTATAGGGATAGTTGTGCAAAGTGAACATTGTAACCTAC  
ACCAACACCTTTAGTACAGTCCCTGCATCCATTCTATTTTAACTTCCATATCTGCCATATTTTACAAAATTTGT  
TCTAGTGCAATTTCCATGGTCCCAATTCATAGTTTATTCATAATGCTATGTCACTATTTTGTAAATGAGGTTTACG  
TTGAAGAAACAGTATACAAGAACCCTGTCTCTCAAATGATCAGACAAAGGTGTTTTGCCAGAGAGATAAAATTTTTG  
CTCAAACCCAGAAAAAGAATTGTAATGGCTACAGTTTCAGTTACTTCCATTTTCTAGATGGCTTTAATTTTGAAAGT  
ATTTTAGTCTGTTATGTTTGTCTTCTATCTGAACAGTTATGTGCCTGTAAAGTCTCCTCTAATATTTAAAGGATTATT  
TTTATGCAAAGTATTCTGTTTCAGCAAGTGCAAATTTTATTCTAAGTTTCAGAGCTCTATATTTAATTTAGGTCAA  
TGCTTTCCAAAAAGTAATCTAATAATCCATTCTAGAAAAATATATCTAAAGTATTGCTTTAGAAATAGTTGTTCCAC  
TTTCTGCTGCAGTATTGCTTTGCCATCTTCTGCTCTCAGCAAGCTGATAGTCTATGTCAATTAATACCCCTATGTT  
ATGTAAGTATGTTATTTTATCCTGTGGTGCATGTTTGGGCAATATATATATAGCCTGATAAACAACTTCTATTAAT  
CAAATATGTACCACAGTGTATGTGTCTTTTGCAAGCTTCCAACAGGGATGTATCCTGTATCATTCATTAAACATAGT  
TTAAAGGCTATCACTAATGCATGTTAATATTGCCTATGCTGCTCTATTTTACTCAATCCATTCTTCACAAGTCTTGG  
TTAAAGATGTCAATATTGGTGATAGAAATGAATTCACCTGCTCTGTCCATTATGTCAAGCAGATAATTTGAAGC  
TATTTACAAACACCTTTACTTTTGCACTTTTAATTCAACATGAGTATCATATGGTATCTCTCTGGATTTCAAGGAAA  
CACACTGGATACTGCCTACTGACAAAACCTATTCTTCATATTTTGCTAAAAATATGTCTAAAACTTGTTTAAATATA  
AATAATGTAAAAATATAATCACTTTATTTGTGAGCATTTTGTACATAAGAAAATTATTTTCAGGTTGATGACATCA  
CAATTTATTTTACTTTATGCTTTTGTCTTTGATTTTTAATCACAATTCCAAACCTTTTGAATCCATAAGATTTTCAA  
TGGATAATTTCTAAATAAAAGTTAGATAATGGGTTTTATGGATTCTTTGTTATAATATATTTTCTACCATTCCA  
ATAGGAGATACATTGGTCAAACACTCAAACCTAGATCATTTTCTACCAACTATGGTTGCCTCAATATAACCTTTTAT  
TCATAGATGTTTTTTTTTATTCAACTTTTGTAGTATTTACGTATGCAGACTAGTCTTATTTTTTAAATCCTGCTGC  
ACTAAAGCTATTACAAATATAACATGGACTTTGTTCTTTTAGCCATGAACAAAGTGGCAAAGTTGTGCAATTACCT  
AACATGATATAAAATTTTGTTTTTTGCAACAAACAAAGTTAATGTTAATTCTTTTTACAAACTATTTACTGTAG  
TGTATTGAAGAACTGCATGCAGGAATTGCTATTGCTAAAAAGAAATGGTGAGCTACGTCAATTATTGAGCCAAAAGAA  
TAAATTTCAATTTTTTATTGCATTTCACTTATTGGGCTCTGGGGTTTTTGTGTTTTGTTTTGCTGTTGGCAGTTTA  
AAATATATATAATTAATAAACCTGTGCTTGATCTGACATTTGTATACATAAAAGTTTACATGAATTTTACAACAA  
CTAGTGCAATGATTACCAAGCAGTACTACAGAACAAAGGCAAATTAAGCAGCTTTGTGAACCTTTTATGTGTGCAA  
AGGATCAAGTTCACATGTTCCAACCTTCAGGTTTGATAATAATAGTAGTAACCACCTACAATAGCTTTCAATTTCAA  
TTAACCCTTGGCTATAAGCATCTAAACTCATCTTCTTTCAATATAATTGATGCTATCTCCTAATTACTTGGTGGC  
TAATAAATGTTACATTCTTTGTACTTAAATGCATTATATAAACTCCTATGTATACATAAGGTATTAATGATATAGT  
TATTGAGAATTTATATTAACTTTTTTTTCAAGAACCCTTGGATTTATGTGAGGTCAAACCAAACTCTTATTCTCAG  
TGGAAAACCTCAGTTGTAATGCATATTTTAAAGACAATTTGGATCTAAATATGTATTTTCAATTTCTCCATAATA  
AATTATATAAGGTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

**FIGURE 80**

AAAAAAATTAAAAAACAGAAAAAACATAGTACATGCCAAGATATTATTATGACAATTACAAAT  
 ACAAATAAATTATGATCTTTGACCTCAGCATATTTATTAATAAGGGAAGATAAACAGGCACATAACTATAACA  
 GGGGCACCAGTCATGGGGCGCCGAGCCGCTCAGGCGCCTCTCGGGCTGCCTGCGGCCTCCGCTCGCCTTCTGCTGCT  
 AGCGACGTTCGGTGCTTCTGCTCTTCGCCTTCTCTCTGCCCCGGAGCCGCGCGTCCAACCAGCCCCGGGTGGTGCG  
 GCGGCACGGGCGGGGACTGTCCCGGCGGCAAAGGCAAGAGCATCAACTGCTCAGAATTAAATGTGAGGGAGTCTGAC  
 GTAAGAGTTTGTGATGAGTCATCATGTAAATATGGAGGAGTCTGTAAAGAAGATGGAGATGGTTTGAAATGTGCATG  
 CCAATTTAGTGCCATACAAATTATATTCCTGTCTGTGGATCAAATGGGGACACTTATCAAATGAATGCTTTCTCA  
 GAAGGGCTGCTTGTAAGCACCAGAAAGAGATAACAGTAATAGCAAGAGGACCATGCTACTCTGATAATGGATCTGGA  
 TCTGGAGAAGGAGAAGAGGAAGGGTCAGGGGCAGAAGTTCACAGAAAACACTCCAAGTGTGGACCTGCAATATAA  
 AGCTGAGTGTGATGAAGATGCAGAAAATGTTGGGTGTGTATGTAATATAGATTGCAGTGGATACAGTTTAAATCCTG  
 TGTGTGCTTCTGATGGGAGTTCCTATAACAATCCCTGTTTTGTTCGAGAAGCATCTTGTATAAAGCAAGAACAAATT  
 GATATAAGGCATCTTGGTCATTGCACAGATACAGATGACACTAGTTTGTGGGAAAGAAAGATGATGGACTACAATA  
 TCGACCAGATGTGAAAGATGCTAGTGATCAAAGAGAAGATGTTTATATTGGAAACCACATGCCTTGCCCTGAAAACC  
 TCAATGGTTACTGCATCCATGGAAAATGTGAATTCATCTATCTACTCAGAAGGGCTTCTTGTAGATGTGAATCTGGC  
 TACACTGGACAGCACTGTGAAAAGACAGACTTTAGTATTCTCTATGTAGTGCCAAGTAGGCAAAAGCTCACTCATGT  
 TCTTATTGCAGCAATTATTGGAGCTGTACAGATTGCCATCATAGTAGCAATTGTAATGTGCATAACAAGAAAATGCC  
 CCAAAAACAATAGAGGACGTCGACAGAAGCAAAACCTAGGTCATTTTACTTCAGATACGTCATCCAGAATGGTTTAA  
 ACTGATGACTTTTATATGTACACTGACCATGTGTATGTACATTTATTATGTCTTTTTTTAAAGAATGGAAATATTTA  
 TTTCAGAAGGCCTTATTTTTGGACATTTTATAGTGTAGTACTGTTGGCTCGATATTTGAATATTCAGCTACGACAGT  
 TTTGGACTGTTTAGTAGTCTTTGTTTTATGTTTTTAAATACAGAAATTGCTTCACAAATTTGTACCACATGGTAATT  
 CTAAGACTTGTCTTTACCCATGGAATGTAATATTTTGCAAAGATGGACTACTTCACAAATGGTTATAAAGTCATA  
 TCCACTTCTTCCACAATGACCACAGCAAATGACCCAAGCATGAACTAAAGAAGAG

**FIGURE 81**

CGCCAGC**ATG**CTGCCGGAGCAGCTCTACTTCCTGCAGAGCCCCCGGAGGAGGAGCCCGAATACCACCCCGACGCCT  
CAGCCCCAAGAATTAAATGTGAGGGAGTCTGACGTAAGAGTTTGTGATGAGTCATCATGTAAATATGGAGGAGTCTGT  
AAAGAAGATGGAGATGGTTTGAAATGTGCATGCCAATTTTCAGTGCCATACAAATTATATTCCTGTCTGTGGATCAAA  
TGGGGACACTTATCAAAATGAATGCTTTCTCAGAAGGGCTGCTTGTAAGCACCAGAAAGAGATAACAGTAATAGCAA  
GAGGACCATGCTACTCTGATAATGGATCTGGATCTGGAGAAGGAGAAGAGGAAGGGTCAGGGGCAGAAGTTCACAGA  
AAACACTCCAAGTGTGGACCCTGCAAATATAAAGCTGAGTGTGATGAAGATGCAGAAAATGTTGGGTGTGTATGTAA  
TATAGATTGCAGTGGATACAGTTTAAATCCTGTGTGTGCTTCTGATGGGAGTTCCTATAACAATCCCTGTTTTGTTC  
GAGAAGCATCTTGTATAAAGCAAGAACAAATTGATATAAGGCATCTTGGTCATTGCACAGATACAGATGACACTAGT  
TTGTTGGGAAAGAAAGATGATGGACTACAATATCGACCAGATGTGAAAGATGCTAGTGATCAAAGAGAAGATGTTTA  
TATTGGAACACATGCCTTGCCCTGAAAACCTCAATGGTTACTGCATCCATGGAAAATGTGAATTCATCTATTCTA  
CTCAGAAGGCTTCTTGTAGATGTGAATCTGGCTACACTGGACAGCACTGTGAAAAGACAGACTTTAGTATTCTCTAT  
GTAGTGCCAAGTAGGCAAAAGCTCACTCATGTTCTTATTGCAGCAATTATTGGAGCTGTACAGATTGCCATCATAGT  
AGCAATTGTAATGTGCATAACAAGAAAATGCCCAAAAACAATAGAGGACGTGACAGAAAGCAAAACCTAGGTCAAT  
TTACTTCAGATACGTCATCCAGAATGGTT**TAA**ACTGATGACTTTTATATGTACACTGACCATGTGATGTACATTAT  
TATGTCTTTTTTTAAAGAATGGAAATATTTATTTTCAGAGGCCTTATTTTTGGACATTTTTAGTGTAGTACTGTTGGC  
TCGTATTTAGAATATTTCAGCTACGACAGTTTTGGACTGTTTAGTAGTCTTTGTTTTATGTTTTTAAATACAGAAAT  
GCTTTCACAAATTTGTACCACATGGTAATTCCTAAGACTTGTCTTTACCCATGGAATGTAATATTTTTGCAAAGATG  
GACTACTTCACAAATGGTTATAAAGTCATATCCACTTCTCCACAATGACCACAGCAAATGACCAAGCATGAACTAA  
AGGTAAAGATGTTTACAGATTACTTTTCTTACAAAAAAATCTAGAAGACACTGTGTTTAAATAGATATTTAAATGT  
TTTTGAGATTTAGTAACTGATTTTTTAGACACTGCCTATCGCATGAACTGTAAAGCTGTGTGTATTAGGTGTAAAT  
ATTTATAAGATATATGGACTGGGGAATTTGATTATTCCTCCCTTTGAAAAAATAGTCCTAATAATTTGAACAAATAT  
GTTAGTAATGATGGAACAGATCAATGAAAAGTAGATATAGATATTGTGAAAATAGGCTGTTTAAACAAACAGATTGGA  
ATAAAGCCTATTCTACCAGTTAACTACTTTAATACACATTCATTTTTAAAGAAAATGTTTGTTTTAACATAAATAA  
ACAAATCGTATCAGTGTGTTGTGAATAAAATACAAAAATGATTGTTAATGATTGGTGCTCTTAAAGTGAGCTTAAAT  
TTATCCAAGACGTATATCCAAATTTGTCCTGTAGTAATAGATTAATATTCATAGATTGTTGGTGTTTAAAGATCTGA  
AGTGTGAGTAGAATGTATTCAGCTGTTTAAACATGTAGTTTAGATATTCAAAAGTATGCATGTAGAATTTAAAGAATA  
TGTTAAAAATTATTAATTTTAATATTTTGTGTTGGAAAAGCATGTTATAATATAATGTTTTCACTATAAAGAAAAAA  
AAAAAAAAAAAA

## **FIGURE 82**

MPTVDDILEQVGESGWFGKQAFLLCLLSAAAFAPICVGIVFLGFTPDHHCQSPGVAELSQRCGWSPAEEELNYTPGL  
 GPAGEAFLGQCRRYEVDWNQSAALSCVDPLASLATNRSHLPLGPCQDGWVYDTPGSSIVTEFNLVCADSWKLDLFQSC  
 LNAGFLFGSLGVGYFADRFGRKLCLLGTVLVNAVSGVLMAFSPNYMSMLLFRLLQGLVSKGNWMAGYTLITEFVGSG  
 SRRTVAIMYQMAFTVGLVALTGLAYALPHWRWLQLAVSLPTFLFLYYWCVPEsprwllsqkrnteaiKIMDHIAQK  
 NGKLPPADLKMLSLEEDVTEKLSPSFADLFRTPLRLKRTFILMYLWFTDSVLYQGLILHMGATSGNLYLDFLYSALV  
 EIPGAFIALITIDRVGRIYPMAMSNLLAGAACLVMIFISPDHLWNIIIMCVGRMGITIAIQMICLVNAELYPTFVR  
 NLGVMVCSSLCDIGGIITPFIVFRLREVWQALPLILFAVLGLLAAGVTLLLPEtkgvalPETMKDAENLGRKAKPKE  
 NTIYLKVQTSEPSGT

Transmembrane domains.

amino acids 19-39, 175-195, 198-218, 235-255, 264-284, 350-370, 377-397,  
 409-429, 457-477, 492-512

N-glycosylation sites.

amino acids 71-74, 96-99, 112-115

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 293-296, 344-347

Tyrosine kinase phosphorylation site.

amino acids 536-544

N-myristoylation sites.

amino acids 76-81, 190-195, 215-220, 231-236, 253-258, 369-374, 389-394,  
 441-446, 465-470, 503-508

Amidation sites.

amino acids 173-176, 531-534

Sugar (and other) transporter homology.

amino acids 118-528

## **FIGURE 83**

MRSDKSALVFLLLQLFCVCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSKPSLIDYRKPSALKFEVV  
HMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFVEIRGTLKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PC  
GDLMAELLAVPFVLT LRISVGGNMERS CGKLPAPLSYVPVPMTGLTDRMTFLERVKN SMLSVLFHFWIQDYDYH FWE  
EFYSKALGRPTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGEDGIVVFSLG  
SLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRYD WIPQNDLLGHPKTKAFITHGGMNGIYEAIYHG  
VPMVGVP IFGDQLDNIAHMKAKGA AVEINFKTM TSEDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWI  
EFVMRHKGAKHLRSA AHDLTWFQHYSIDVIGFLLTCVATAIFLFTKCF LFSCQKFNKTRKIEKRE

Signal sequence.

amino acids 1-21

Transmembrane domain.

amino acids 489-509

N-glycosylation sites.

amino acids 131-134, 313-316, 518-521

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 67-70, 340-343

Tyrosine kinase phosphorylation sites.

amino acids 122-131, 136-144

N-myristoylation sites.

amino acids 19-24, 276-281, 373-378, 377-382

Amidation site.

amino acids 338-341

## **FIGURE 84**

MQADARAFFAQDGVQSLLTQKWWGDMASSTPIWALVLAFFCPPLIYTRLITFRKSEEEPTREELEFDMDSVINGEGP  
 VGTADPAEKTPLGVPRQSGRPGCCGGRCGGRRCLRRWFHFWGAPVTIFMGNVVSYLELLLFSSRVLLVDFQPAPPGS  
 LELLLYFWAFTLLCEELRQGLSGGGGSLASGGPGPGHASLSQRLRLYLADSWNQCDLVALTCFLLGVGCRLTPGLYH  
 LGRTVLCIDFMVFTVRLRHIFTVNKQLGPKIVIVSKMMKDVFFFLFGLGVWLVA YGVATEGLLRPRSDFPSILRRV  
 FYRPLYQIFGQIPQEDMDVALMEHSNCSSEPGFWAHPPGAQAGTCVSQYANWLVLVLLLVIFLLVANILLVNLLIAMF  
 SYTFGKVQGNSDLYWKAQVTASSGNSTLGPRWPRPLSSSPTCASC SGNCAGDPGAPSRPPRPSSISGFTFLRKPSGS  
 ANVGIGA

Transmembrane domains.

amino acids 26-46, 118-138, 203-223, 233-253, 269-289, 358-378

N-glycosylation sites.

amino acids 334-337, 410-413

Glycosaminoglycan attachment site.

amino acids 176-179

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 457-460

N-myristoylation sites.

amino acids 99-104, 102-107, 106-111, 119-124, 127-132, 174-179, 177-182, 179-  
 184, 180-185, 347-352, 351-356, 432-437

Amidation site.

amino acids 106-109

Leucine zipper pattern.

amino acids 211-232

## **FIGURE 85**

MTLWNGVLPFYPPQRHAAGFSVPLLIVFLALAASFLLILPGIRGHSRWFVLVRVLLSLFIGAEIVAVHFSAEWF  
VGTVNTNTSYKAFSAARVTARVGLLVGLEGINITLTGTPVHQLNETIDYNEQFTWRLKENYAAEYANALEKGLPDPV  
LYLAEKFTPSSPCGLYHQYHLAGHYASATLWVAFCFWLLSNVLLSTPAPLYGGLALLTTGAFALFGVFALASISSVP  
LCPLRLGSSALTTQYGAAFWVTLATGVLCFLGGAVVSLQYVRPSALRTLDDQSAKDCSQERGGSPILIGDPLHKQA  
ALPDLKCITTNL

Transmembrane domains.

amino acids 19-39, 54-74, 94-114, 178-198, 211-231, 251-271

N-glycosylation sites.

amino acids 84-87, 109-112, 121-124

Tyrosine kinase phosphorylation site.

amino acids 148-157

N-myristoylation sites.

amino acids 79-84, 100-105, 107-112, 265-270

Leucine zipper pattern.

amino acids 197-218



**FIGURE 86**

MERLWGLFQRAQQLSRSSQTVYQRVEGPRKGHLEEEEDGEEGAETLAHFCEMELRGPEPLGSRPRQPNLIPWAAA  
GRRAAPYLVLTAALLIFTGAFLLGYYAFRGSCQACGDSVLVSEVDVNYEPDLDFHQGRLYWSDLQAMFLQFLGEGRL  
DTIRQTSLRERVAGSAGMAALTQDIRAALSQKLDHVWTDTHYVGLQFPDPAHPNTLHWVDEAGKVGEQLPLEDPDV  
YCPYSAIGNVTGELVYAHYGRPEDLQDLRARGVDPVGRLLLVRVGVISFAQKVTNAQDFGAQGVLIYPEPADFSQDP  
PKPSLSSQQAVYGHVHLGTGDPYTPGFPSFNQTQFPVASSGLPSIPAQPIASDIASRLRLKLGKPVAPQEWQGSLL  
GSPYHLGPGPRLRLVNNHRTSTPINNIFGCI EGRSEPDHYVVIGAQRDAWGPGAASAVGTAILLELVRTFSSMVS  
NGFRPRRSLLFISWDGGDFGSVGSTEWLEGYLSVLHLKAVVYVSLDNAVLGDDKFHAKTSPLLTSLIESVLKQVDS  
NHSGQTLYEQVVFNTNPSWDAEVIRPLPMDSSAYSFTA FVGVPAVEFSFMEDDQAYPFLHTKEDTYENLHKVLQGR  
LPAVAQAVAQLAGQLLIRLSHDLRLPLDFGRYGDVVL RHIGNLNEFSGDLKARGTLQWVYSARGDYIRAAEKL  
RQEIY SSEERDERLTRMYNVRIMRVEFYFLSQYVSPADSPFRHIFMGRGDHTLGALLDHLRLRLRSNSSGTPGAT  
SSTGFQES RFRRLALLTWTLQGAANALSGDVWNIDNNF

Transmembrane domain.

amino acids 79-99

N-glycosylation sites.

amino acids 240-243, 339-342, 540-543, 754-757

N-myristoylation sites.

amino acids 106-111, 239-244, 382-387, 415-420, 439-444, 478-483, 482-487, 757-  
762, 760-765, 785-790

Amidation site.

amino acids 77-80

Cell attachment sequences.

amino acids 678-680, 736-738

PA domain.

amino acids 236-335

## **FIGURE 87**

MVELMFLLLLLLPFLLYMAAPQIRKMLSSGVCTSTVQLPGKVVVVTGANTGIGKETAKELAQRGARVYLACRDVEK  
GELVAKEIQTTTGNQQVLVRKLDLSDTKSIRAFAGFLAEEKHLHVLINNAGVMMCPYSKTADGFEMHIGVNH LGHF  
LLTHLLEKLKESAPSRIVNVSSLAHHLGRIHFHNLQGEKFYNAGLAYCHSKLANILFTQELARRLKSGVTTYSVH  
PGTVQSELVRHSSFMRRWWLFSFFIKTPQGAQTSLHCALTEGLEILSGNHFS DCHVAWVSAQARNETIARRLWDV  
SCDLLGLPID

Signal sequence.

amino acids 1-20

Transmembrane domain.

amino acids 32-52

N-glycosylation sites.

amino acids 174-177, 298-301

N-myristoylation sites.

amino acids 31-36, 48-53, 199-204, 222-227, 233-238, 263-268, 281-286

Short chain dehydrogenase.

amino acids 40-303

## **FIGURE 88**

MKIFLPVLLAALLGVERASSLMCFSCLNQKSNLYCLKPTICSDQDNYCVTVSASAGIGNLVTFGHSLSKTCSPACPI  
PEGVNVGVASMGISCCQSFLCNFSAADGGLRASVTLLGAGLLLSLLPALLRFGP

Signal sequence.

amino acids 1-20

Transmembrane domain.

amino acids 108-128

N-glycosylation site.

amino acids 99-102

N-myristoylation sites.

amino acids 14-19, 58-63, 80-85, 89-94, 105-110, 106-111, 117-122

u-PAR/Ly-6 domain.

amino acids 21-100

## **FIGURE 89**

MLLLKKHTEDISSVYEIRERLGSFSEVVLAQERGSAPHLVALKCIPKKALRGKEALVENEIAVLRRISHPNIVALE  
DVHESPSHLYLAMELVTTGGELFDRIMERGSYTEKDASHLVGQVLGAVSYLHSLGIVHRDLKPENLLYATPFEDSKIM  
VSDFGLSKIQAGNMLGTACGTPGYVAPELLEQKPYGKAVDVWALGVISYILLCGYPPFYDESDPELFSQILRASYES  
DXPFWDDISESGKDFIRHLLERDLQKRFTCQQALRDLWIFWDTGFGRDILGFVSEQIRKNFAWTHWKRAFNATLFLR  
HIRKLGQIPEGEGASEQGMXRSHXGLRAGQPPKW

N-glycosylation site.

amino acids 302-305

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 5-8, 66-69, 257-260

Tyrosine kinase phosphorylation site.

amino acids 101-109

N-myristoylation sites.

amino acids 118-123, 166-171, 170-175, 334-339

Serine/Threonine protein kinases active-site signature.

amino acids 132-145

Protein kinase domain.

amino acids 15-270

## **FIGURE 90**

MEELQDDYEDMMEENLEQEEYEDPDI PESQMEEPAAHDTEATATDYHTTSHPGTHEVYVELQELVMDEKNQELRWME  
AARWVQLEENLGENGAWGRPHLSHLTFWSLLELRRVFTKGTVLLDLQETSLAGVANQLLDRFIFEDQIRPQDREELL  
RALLLKHSHAGELEALGGVKPAVLTRSGDPSQPLL PQHSSLETQLFCEQGDGGTEGHSPSGILEKIPPDSEATLVLV  
GRADFLEQPVLG FVRLQEAAELEAVELPVPIRFLFVLLGPEAPHIDYTQLGRAAAATLMSERVFRIDAYMAQSRGELL  
HSLEGFLDCSLVLPPTDAPSEQALLSLVPVQRELLRRRYQSSPAKPDSSFYKGLDINGGPDDPLQQTGQLFGGLVRD  
IRRRYPYYLSDITDAFSPQVLA AVIFIYFAALSPAITFGG LLGEKTRNQMGVSELLISTAVQGILFALLGAQPLL VV  
GFSGPLL VFEEAFFSFCETNGLEYIVGRVWIGFWLILLVVLV VAFEGSFLVRFISRYTQEIFSFLISLIFIYETFSK  
LIKIFQDHPLQKTYNNVLMV PKPQGPLPNTALLSLVLMAGTFFFAMMLRKFKNSSYFPGKLRRVIGDFGVPI SILI  
MVLVDFFIQD TYTQKLSVPDGFKVSNS SARGWVIHPLGLRSEFFIWM MFASALPALLVFILIFLESQITTLIVSKPE  
RKMVKGSGFHLDLLLVGMGGVAALFGMPWLSATTVR SVTHANALTVMGKASTPGAAAQIQEVKEQRISGLLVAVLV  
GLSILMEPILSRIPLAVLFGIFLYMGVTSLSGIQLFDRILL LFKPPKYHPDVPYVKRVKVTWRMHLFTGIQIICLAVL  
WVVKSTPASLALPFVLILT VPLRRVLLPLIFRNVELQCLDADDAKATFDEEEGRDEYDEVAMPV

Transmembrane domains.

amino acids 401-421, 445-465, 487-507, 519-539, 564-584, 602-622, 663-683, 700-720, 761-781, 793-813, 831-851, 854-874

N-glycosylation site.

amino acids 593-596, 642-645

Tyrosine kinase phosphorylation site.

amino acids 817-824

N-myristoylation sites.

amino acids 172-177, 206-211, 361-366, 376-381, 424-429, 448-453, 609-614, 713-718, 763-768

Anion exchangers family signature 1.

amino acids 379-390

Anion exchangers family signature 2.

amino acids 526-540

## **FIGURE 91**

MVAWVSTGVAIACCAAVYYLAEYNLEFLKTHSNPGAVLLLPFVVSCLAVPCISMFRLVERYEMPRHEVYVLLI  
RNIFLKISIIIGILCYWLNLTVALSGEECWETLIGQDIYRLLLMDFVFSLVNSFLGEFLRRIIGMQLITSLGLQEFDI  
ARNVLELIYAQTLVWIGIFFCPLLPFIQMIMLFIMFYSKNISLMMNFQPPSKAWRASQMMTFFIFLLFFPSFTGVLC  
TLAITIWRLKPSADCGPFRGLPLFIHSIYSWIDTLSTRPGYLWVWVIYRNLIGSVHFFFIITLIVLIITYLYWQITE  
GRKIMIRLLHEQIINEGKDKMFLIEKLIKLDMEKKANPSSLVLERREVEQQGFLHLGEHDGSLDLRSRRSVQEGNPRA

Transmembrane domains.

amino acids 1-16, 34-54, 75-95, 114-134, 159-179, 175-195, 213-233, 250-270,  
281-301

N-glycosylation site.

amino acids 194-197

Tyrosine kinase phosphorylation site.

amino acids 156-163

N-myristoylation sites.

amino acids 9-14, 228-233

Amidation site.

amino acids 308-311

## **FIGURE 92**

MERRRLWGSIQSRYISMSVWTSPPRLVELAGQSLLKDEALIAALELLPRELFPPLFMAAFDGRHSQTLKAMVQAWP  
FTCLPLGVLMKGQHLHLETFAVLDGLDVLLAQEVRRRWKLQVLDLRKNSHQDFWTVWSGNRASLYSFPEPEAAQP  
MTKKRKVDGLSTEAEQPFIPVEVLVDLFLKEGACDELFSYLIEKVRRKKNVRLCCKKLIKIFAMPMDIKMILKMVQ  
LDSIEDLEVTCTWKLPTLAKFSPYLGQMINLRRLLSHIHASSYISPEKEEQYIAQFTSQFLSLQCLQALYVDSLFF  
LRGRDQLLRHVMNPLETLSITNCRLSEGDVMHLSQSPSVSQSVLSLGVMLTDVSPEPLQALLERASATLQDLVF  
DECGITDDQLLALLPSLSHCSQLTTLSFYGNSISISALQSLQHLIGLSNLTHVLYPVPLESYEDIHGTLHLERLAY  
LHARLRELLCELGRPSMVWLSANPCPHCGDRTFYDPEPILCPCFMPN

N-glycosylation site.

amino acids 435-438

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 125-128

N-myristoylation sites.

amino acids 8-13, 138-143, 257-262, 358-363, 415-418

**FIGURE 93**

MTQRSIAGPICNLKFVTLLVALSSELPFLGAGVQLQDNGYNGLLIAINPQVPENQNLISNIKEMITEASFYLFNATK  
 RRVFFRNKILIPATWKANNNSKIKQESYEKANVIVTDWYGAGHDDPYTLQYRGCGKEGKYIHFTPNFLLNDNLTAG  
 YGSRGRVVFHEWAHLRWGVFDEYINDKPFYINGQNQIKVTRCSSDITGIFVCEKGPCPQENCIISKLFKEGCTFIYN  
 STQNATASIMFMQSLSSVVEFCNASTHNQEAPNLQNQMCSLRSAWDVITDSADFHHSFPMNGTELPPTTFSLVQAG  
 DKVVCLVLDVSSKMAEADRLQLQQAEEFYLMQIVEIHTFVGIAFDSKGEIRAQLHQINSNDDRKLLVSYLPTTVS  
 AKTDISICSGLKKGFVVEKLNKAYGSVMILVTSGDDKLLGNCLPTVLSSGSTIHSIALGSSAAPNLEELSRLTGG  
 LKFFVPDISNSNSMIDAFSRISSTGDIQQHIQLESTGENVKPHHQLKNTVTVDNTVGNDTMFLVTWQASGPPEII  
 LFDPDGRKYTNNFITNLTFRTASLWIPGTAKPGHWYTLNNTHHSLQALKVTVTSRASNSAVPPATVEAFVERDSL  
 HFPHVPMIYANVKQGFYPILNATVTATVEPETGDPVTLRLRDDGAGADVIKNDGIYSRYFFSFAANGRYSLKVHVNH  
 SPSISTPAHSIPGSHAMYVPGYTANGNIQMNAPRKSVGRNEEERKWGFSRVSSGGSFSVLGVPAGPHPDVFPCKII  
 DLEAVKVEEELTSLWTAPGEDFDQQAQTSYEIRMSKSLQNIQDDFNNAILVNTSKRNPQQAGIREIFTFSPQISTNG  
 PEHQPNGETHESHRIYVAIRAMDRLSLQSAVSNIQAPLFIPPNSDPVPARDYLILKGVLTAAGLIGIICLIIVVTH  
 HTLSRKKRADKKENGTKLL

Signal sequence.

amino acids 1-31

Transmembrane domain.

amino acids 903-923

N-glycosylation sites.

amino acids 74-77, 97-100, 150-153, 231-234, 235-238, 254-257, 292-295, 522-525,  
 556-559, 580-583, 637-640, 822-825, 938-941

Glycosaminoglycan attachment site.

amino acids 485-488

N-myristoylation sites.

amino acids 42-47, 202-207, 395-400, 747-752, 795-800, 905-910

Amidation site.

amino acids 544-547



## **FIGURE 94**

MALNSGSPPAIGPYYENHGYQPENPYPAQPTVVPTVYEVHQAQYYPSVPQYAPRVLTQASNPVVCTQPKSPSGTVC  
TSKTKKALCITLTLGTFLVGAAALAGLLWKFMGSKCSNSGIECDSSGTCINPSNWCDGVSHCPGGEDENRCVRLYGP  
NFILQMYSSQRKSWHPVCQDDWNENYGRAACRDMGYKNNFYSSQGI VDDSGSTSFMKLNTSAGNVDIYKKLYHSDAC  
SSKAVVSLRCLACGVNLNSSRQSRIVGGESALPGAWPWQVSLHVQNVHVCGGSIIITPEWIVTAAHCVEKPLNNPWHW  
TAFAGILRQSFMFYGAGYQVQKVISHPNYDSKTKNNDIALMKLQKPLTFNDLVKPVCLPNPGMMLQPEQLCWISGWG  
ATEEKGKTSEVLNAAKVLLIETQRCNSRYVDNLITPAMICAGFLQGNVDSCQGDSSGGLVTSNNNIWWLIGDTSWG  
SGCAKAYRPGVYGNVMVFTDWIYRQMKANG

Transmembrane domain.

amino acids 86-106

N-glycosylation sites.

amino acids 213-216, 249-252

Glycosaminoglycan attachment site.

amino acids 382-385

N-myristoylation sites.

amino acids 6-11, 74-79, 97-102, 110-115, 245-250, 258-263, 432-437, 462-467,  
464-469, 472-477

ATP/GTP-binding site motif A (P-loop).

amino acids 386-393

Serine proteases, trypsin family, histidine active site.

amino acids 292-297

Trypsin homology.

amino acids 256-484

**FIGURE 95**

MARSLLLPLQILLLSLALETAGEEAQGDKIIDGAPCARGSHPWQVALLSGNQLHCGGVLVNERWVLTAAHCKMNEYT  
VHLGSDTLGDRRAQRIKASKSFRHPGYSTQTHVNDLMLVKLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTS  
PDVTFPSDLMCVDVKLISPQDCTKVYKDLENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQPNP  
PGVYTQVCKFTKWINDTMKKHR

Signal sequence.  
amino acids 1-15

N-glycosylation site.  
amino acids 246-249

Glycosaminoglycan attachment site.  
amino acids 147-150

N-myristoylation sites.  
amino acids 33-38, 57-62, 141-146, 192-197, 213-218, 222-227

Serine proteases, trypsin family, histidine active site.  
amino acids 66-71

Trypsin homology.  
amino acids 30-245

**FIGURE 96**

MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLLHLHQTAAHADEFDCPSELQHTQELFPQWHLPIKI  
AAIIASLTFLYTLREVIHPLATSHQQYFYKIPILVINKVLPVMSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWL  
DKWMLTRKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHADVWRMEIYVSLGIVGLAILA  
LLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIKFSIL  
FLPCLRKKILKIRHGWEDVTKINKTEICSQL

Transmembrane domains.

amino acids 72-92, 116-136, 158-178, 218-238, 254-274, 291-311

N-glycosylation sites.

amino acids 143-146, 331-334

Tyrosine kinase phosphorylation site.

amino acids 19-27

N-myristoylation sites.

amino acids 133-138, 265-270

## **FIGURE 97**

MDSSPSLPLIRTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESMYHSLTYATILEMQAMMTFDPQDILLA  
GNMMKEAQMLCQRHRRKSSVTDSFSSLVNRPTLGQFTEEEIHAEVCYAECLLQRAALTFLQGSSHGGAVRPRALHDP  
SHACSCPPGPRQHLFLLQDENMVSFYKGGIKVRNSYQTYKELDSLQSSQYCKGENHPHFEGGVKLGVGAFNLTL  
MLPTRILRLLEFVGFSGNKDYGLLQLEEGASGHSFRSVLCVMLLLCYHTFLTFTVLGTGNVNIEEAELLLKPYLNRY  
KGAIFLFFAGRIEVIKGNIDAVSDGGPGRGWGSLGVSQTSRKSGTCDILRDRIDWGRGGGQERTNQ RAGAGEALLAE  
QPGKTREEEAFVVPGILTGRYRTAALQWREVEGGA

Transmembrane domain.

amino acids 267-287

N-glycosylation site.

amino acids 227-230

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 92-95, 93-96

Tyrosine kinase phosphorylation site.

amino acids 46-52

N-myristoylation sites.

amino acids 139-144, 218-223, 325-330, 343-348, 368-373, 377-382, 400-405

Eukaryotic putative RNA-binding region RNP-1 signature.

amino acids 309-316

## **FIGURE 98**

MADAEVIILPKKHKKKKKERKSLPEEDVAEIQHAEFLIKPESKVAKLDTSQWPLLLKNFDKLNVRTTHYTPLACGSN  
PLKREIGDYIRTGFINLDKPSNPSSHEVVAWIRRIILRVEKTGHSGTLDPKVTGCLIVCIERATRLVKSQQSAGKEYV  
GIVRLHNAIEGGTQLSRALETLTGALFQRPPLIAAVKRQLRVRTIYESKMIEDPERRLGIFWVSCEAGTYIRTL CV  
HLGLLLGVGGMQELRRVRSGVMSEKDHMTMHDVLD AQWLYDNHKDESYLRRVVYPLEKLLTSHKRLVMKDSAVNA  
ICYGAKIMLPGLVRYEDGIEVNQEIVVITTKGEAICMAIALMTTAVISTCDHGIVAKIKRVIMERDTYPRKWGLGPK  
ASQKKLMIKQGLLDKHGKPTDSTPATWKQEYVDYSES AKKEVVAEVVKAPQVVAEAAKTAKRKRESESESEDET PPAA  
PQLIKKEKKKSKDKKAKAGLESGAEPGDGSDTTKKKKKKKKAKEVELVSE

Transmembrane domain.

amino acids 220-240

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 448-451, 470-473

Tyrosine kinase phosphorylation site.

amino acids 368-376

N-myristoylation sites.

amino acids 166-171, 234-239, 326-331, 482-487, 486-491

TruB family pseudouridylate synthase homology.

amino acids 107-247

PUA domain.

amino acids 295-370

**FIGURE 99**

MALRICVTYTPALPIGLCTRCCLEQSPSWCHCLRGVSFLTFFHLHQSVPLGDRDSLMMFTRQAGHFVEGSKAGRSR  
GRLCLSQALRVAVRGAFVSLWFAAGAGDRERNKGDKGATGAGLSQEAEDVDVSRARRVTDAPQGTLCGTGNRNSGS  
QSARAVGVVAHLGEAFRVGVEQAISSCPEEVHGRHGLSMEIMWARMDVALRSPGRGLLAGAGALCVTLAESSCPDYER  
GRRACLTLLHRHPTPHCSTWGLPLRVAGSWLTVVTVEALGGWRMGVVRTGQVGPTMHPPPVS GASPLLLHLLLLLLLI  
IILTC

Signal sequence.

amino acids 1-34

Transmembrane domains.

amino acids 80-100, 250-270, 293-312

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 134-137

N-myristoylation sites.

amino acids 70-75, 92-97, 114-119, 118-123, 142-147, 148-153, 153-158, 172-177,  
209-214, 258-263, 275-280

Amidation site.

amino acids 231-234

Eukaryotic putative RNA-binding region RNP-1 signature.

amino acids 36-43

**FIGURE 100**

MGIVANFQELAVPVVHDGGALLAFVCGVVYTLLQSIISYKSCPQWNSLSTCHIRMVISAVSAAVIPMIVCASLISI  
TKLEWNPREKDYVYHVVSAICEWTVAFGFIFYFLTFIQDFQSVTLRISTEINGDI

Transmembrane domains.

amino acids 10-30, 53-73, 93-113

Tyrosine kinase phosphorylation site.

amino acids 85-91

N-myristoylation sites.

amino acids 2-7, 19-24, 27-32

## **FIGURE 101**

MPRQLSAAAAALFASLAVILHDGSQMRKAFFPETRDYSQPTAAATVQDIKKPVQQPAKQAPHQTLAARFMDGHITFQT  
AATVKIPTTTTPATTKNTATTSPITYTLVTTQATPNNSTAPPVTEVTVGPSLAPYSLPPTITPPAHTAGTSSSTVSH  
TTGNTTQPSNQTTLPATLSIALHKSTTGQKPDQPTHAPGTAAAHNTTRTAAPASTVPGPTLAPQPSSVKTGIYQVL  
NGSRLCIKAEMGIQLIVQDKESVFSPPRYFNIDPNATQASGNCGTRKSNLLLNFQGGFVNLTFTKDEESYYISEVGA  
YLTVSDPETVYQGIKHAVVMFQTAVGHSFKCVSEQSLQLSAHLQVKTTDVQLQAFDFEDDHFGNVDECSSDYTIVLP  
VIGAIVVGLCLMGMGVYKIRLRCQSSGYQRI

Signal sequence.

amino acids 1-16

Transmembrane domain.

amino acids 380-400

N-glycosylation sites.

amino acids 112-115, 158-161, 164-167, 200-203, 232-235, 266-269, 291-294

Tyrosine kinase phosphorylation sites.

amino acids 28-36, 296-302

N-myristoylation sites.

amino acids 146-151, 193-198, 233-238, 272-277, 275-280, 287-292, 307-312, 321-326

Lysosome-associated membrane glycoprotein homology.

amino acids 66-416



**FIGURE 102**

MTEEPIKEILGAPKAHMAATMEKSPKSEVVITTVPLVSEIQLMAATGGTELSYRCIIPFAVVVFIAGIVVTAVAYS  
FNSHGSIIISIFGLVVLSSGLFLLASSALCWKVRQRSKKAKRRESQTALVANQORSLFA

Transmembrane domains.

amino acids 54-74, 84-104

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 118-121

N-myristoylation sites.

amino acids 11-16, 48-53, 68-73, 82-87

## **FIGURE 103**

MLSLHASTLAVLGALCVYGAGHLEQFPQISSTKTLSTARLECVVSGITISATSVYWYRERPGEVIQFLVSISYDGT  
VRKESGIPSGKFEVDRIPESTSTLTIHNVKQDIATYYCALWEVRLANQELGKKIKVFGPGTKLIITDKQLDADVS  
PKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIKIHWEKKSNTILGSQEGNTMKTNDTYMKFSWLTVPKSLDKEH  
RCIVRHENNKNGVDQEIIFFPIKTDVITMDPKDNCSKDANDTLLLQLTNTSAYYTYLLLLLKSVVYFAIITCCLLR  
TAFCCNGEKS

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 282-302

N-glycosylation sites.

amino acids 211-214, 265-268, 271-274, 280-283

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 79-82

N-myristoylation sites.

amino acids 47-52, 83-88, 173-178, 201-206

Amidation site.

amino acids 129-132

Immunoglobulin domain.

amino acids 36-119

## **FIGURE 104**

MNYSLHLAFVCLSLFTERMCIQGSQFNVEVGRSDKLSLPGFENLTAGYNKFLRPNFGGEPVQIALTLDIASISSISE  
 SNMDYTATIYLRQRWMDQRLVFEGNKSFTLDARLVEFLWVPDTYIVESKKSFLHEVTVGNRLIRLFSNGTVLYALRI  
 TTTVACNMDLSKYPMDTQTCKLQLESWGYDGNDVEFTWLRGNDSVRGLEHLRLAQYTIERYFTLVTRSQQETGNYTR  
 LVLQFELRRNVLYFILETYVPSTFLVLSWVSFWISLDSVPARTCIGVTTVLSMTTLMIGSRTSLPNTNCFIKAIDV  
 YLGICFSFVFGALLEYAVAHYSSLQQMAAKDRGTTKEVEEVSITNIINSSISSFKRKISFASIEISSDNVDYSDLTM  
 KTS DKFKFVFREKMGRIVDYFTIQNPSNVDHYSKLLFPLIFMLANVFYWAYMYF

Signal sequence.

amino acids 1-16

Transmembrane domains.

amino acids 306-326, 415-435

N-glycosylation sites.

amino acids 2-5, 43-46, 102-105, 145-148, 196-199, 228-231, 356-259

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 364-367

Tyrosine kinase phosphorylation sites.

amino acids 175-183, 221-229

N-myristoylation sites.

amino acids 23-28, 291-296, 311-316

Neurotransmitter-gated ion-channels signature.

amino acids 160-174

Neurotransmitter-gated ion-channel ligand binding domain.

amino acids 37-242

Neurotransmitter-gated ion-channel transmembrane region.

amino acids 249-434

## **FIGURE 105**

MILVLLCAFLIPCPRDLHSTWSRHLGSQGGGDLSPLELADVNGDGLRDVLLSFVMSRNGSAVGVSIPAANLVCLSG  
MNGSTLWSSLLPEEARDITCLELMPGSLAETICLVGTGTHKMLSAFNATSGKAIWTLNPNYLSNGTLAAPVVVLPDL  
EDGVRDLVVLAIQELQPDLCFLLVSGRTGNPVGPRVKYNIVGVGNLIGPQVYITNGAVYILFGFGNIQAVLRDIF  
VQAQNRDSSPPSLQIEEPEWEKRRSINLSELIDVYSDGVVELLQMVKAPDSNCSNLLITRQSLVLLRGQNLTPYWAL  
RLQGLRSQPTPGYFTDDQTLDFLLQIQDGVGMKMMVVDGSGSIVWSYRAPCHMKETPATSAVTSQKSVFLFWAE  
GLSAASPNSDIILGTEPPSLHHLYLLHPAFPSILLDLANTTGTVTASEVGINDLWKDAFYVTRTTGPSSEGHPAALV  
VSKLSLRWALMEGQMAQLQESTPKIGRGELRRFLSRIKFVEAPYEI

Signal sequence.

amino acids 1-15

Transmembrane domain.

amino acids 202-222

N-glycosylation sites.

amino acids 59-62, 79-82, 123-126, 140-143, 258-261, 282-285, 424-427

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 253-256

Tyrosine kinase phosphorylation site.

amino acids 500-506

N-myristoylation sites.

amino acids 27-32, 60-65, 77-82, 183-188, 220-225, 386-391, 427-432

**FIGURE 106**

MSNKFLGTWKLVSSENFDDYMKALGVGLATRKLGNLAKPTVIISKKGDIITIRTESTFKNTEISFKLGQEFEEETAD  
NRKTKSIVTLQRGSLNQVQRWDGKETTIKRKLVNGKMVAECKMKGVVCTRIYEV

N-myristoylation sites.

amino acids 25-30, 122-127

Lipocalin/cytosolic fatty-acid binding protein homology.

amino acids 4-132

## **FIGURE 107**

MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGLALALEPALASPAGAANF  
 LAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHYSYIDTYFDTERSSTYRSKGFDTVVKYTQGSW  
 TGFVGEDLVTIPKGFNTSFLVNIATIFESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQ  
 MCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDGREYNADKAIVDSGTTT  
 LRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSSRSFRITILPQLYIQPMM  
 GAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAETAGAAVSEISGPFSTEDVASNCVPAQS  
 LSEPILWIVSYALMSVCGAILLVLLVLLLPPFCQRRPRDPEVVNDESSLVRHRWK

Signal sequence.

amino acids 1-20

Transmembrane domain.

amino acids 471-491

N-glycosylation sites.

amino acids 170-173, 366-369

Glycosaminoglycan attachment site.

amino acids 88-91

N-myristoylation sites.

amino acids 59-64, 120-125, 152-157, 190-195, 198-203, 236-241, 241-246, 243-  
 248, 253-258, 285-290, 339-344, 386-391, 397-396, 438-443

Leucine zipper patterns.

amino acids 10-31, 197-218

Eukaryotic aspartyl protease homology.

amino acids 41-431

## **FIGURE 108**

MAVKLGTL L L L L A L G L A Q P A S A R R K L L V F L L D G F R S D Y I S D E A L E S L P G F K E I V S R G V K V D Y L T P D F P S L S Y P N Y Y T  
L M T G R H C E V H Q M I G N Y M W D P T T N K S F D I G V N K D S L M P L W W N G S E P L W T L T K A K R K V Y M Y W P G C E V E I L G V R P T Y C  
L E Y K N V P T D I N F A N A V S D A L D S F K S G R A D L A A I Y H E R I D V E G H H Y G P A S P Q R K D A L K A V D T V L K Y M T K W I Q E R G L Q D  
R L N V I I F S D H G M T D I F W M D K V I E L N K Y I S L N D L Q Q V K D R G P V V S L W P A P G K H S E I Y N K L S T V E H M T V Y E K E A I P S R F  
Y Y K K G K F V S P L T L V A D E G W F I T E N R E M L P F W M N S T G R R E G W Q R G W H G Y D N E L M D M R G I F L A F G P D F K S N F R A A P I R S  
V D V Y N V M C N V G I T P L P N N G S W S R V M C M L K G R A G T A P P V W P S H C A L A L I L L F L L A

Signal sequence.

amino acids 1-22

Transmembrane domain.

amino acids 423-439

N-glycosylation sites.

amino acids 100-103, 118-121, 341-344, 404-407

Tyrosine kinase phosphorylation sites.

amino acids 191-199, 251-258

N-myristoylation sites.

amino acids 148-153, 365-370

Amidation site.

amino acids 343-346

Phosphodiester Type I phosphodiesterase.

amino acids 5-381

**FIGURE 109**

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTATTAASTTARKDIPVLP  
KWVGDLPNGRVCP

Signal sequence.  
amino acids 1-19



## **FIGURE 110**

MFQTGGLIVFYGLLAQTM AQFGGLPVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDIL  
KPGGGTSGGLLGGLLGKVT SVIPGLNNIIDIKVTD PQLLELGLVQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLA  
VKLDITAEILAVRDKQERIHVLVGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILNKVLP ELVQGNVCPLVNEVL  
RGLDITLVH DIVNMLIHGLQFVIKV

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 134-154

N-myristoylation sites.

amino acids 46-51, 49-54, 58-63, 62-67, 66-71, 80-85, 81-86, 82-87, 85-90, 86-91, 89-94, 202-207, 233-238

**FIGURE 111**

MEPPYSLTAHYDEFQEVKYVSRGAGGARGASLPFGFPLGAARSVTGARSGLPRWNRREVCLLSGLVFAAGLCAILA  
 AMLALKYLGPVAAAGGGACPEGCPEKAFARAARFLAANLDASIDPCQDFYSFACGGWLRRAIPDDKLTGTIAAIG  
 EQNEERLRLLARPGGGPGGAAQRKVRAFFRSCLDMREIERLGPRPMLEVEDCGGWDLGGAEEERPGVAARWDLNRL  
 LYKAQGVYSAAALFSLTVSLDDRNSSRYVIRIDQDGLTLPERTLYLAQDEDSEKILAAAYRVFMERVLSSLGADAVEQ  
 KAEILQVEQQLANITVSEYDDLRRDVSSMYNKVTLGQLQKITPHLRWKWLLDQIFQEDFSEEEVLLATDYMQQV  
 SQLIRSTPHRVLHNYLVWRVVVLSEHLSPPFREALHELAQEMEGSDKPQELARVCLGQANRHFGMALGALFVHEHF  
 SAASKAKVQQLVEDIKYILGQRLEELDWMDAETRAAARAKLQYMMVMVGYPDFLLKPDVDKEYEFVHEKTYFKNI  
 LNSIPFSIQLSVKKIRQEVDKSTWLLPPQALNAYYLPNKNQMVFPAGILQPTLYDPDFPQSLNYGGIGTIIGHELTH  
 GYDDWGGQYDRSGNLLHWWTEASYSRFLRKAECIVRLYDNFTVYNQVRNGKHTLGENIADMGVCLKLAYHAYQKWVRE  
 HGPEHPLPRLKYTHDQLFFIAFAQNWCIKRRSQSIYLQVLTDKHAPEHYRVLGVSVSQFEEFGRAFHCPKDSMPNPAH  
 KCSVW

Transmembrane domain.

amino acids 64-84

N-glycosylation sites.

amino acids 255-258, 322-325, 656-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 722-725

N-myristoylation sites.

amino acids 24-29, 26-31, 27-32, 40-45, 47-52, 65-70, 148-153, 169-174, 170-175,  
 237-242, 450-455, 604-609, 607-612

Prenyl group binding site (CAAX box).

amino acids 772-777

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 609-618

Peptidase family M13.

amino acids 571-774

## **FIGURE 112**

MGPSCPVLFSFTKLSLWLLLLTPAGGEEAKRPPPPRAPGDPLSSPSPTALPQGGSHTEDETDLFKHLFRGYNRWARPV  
PNTSDVVIVRFGLSIAQLIDVDEKNQMMTTNVWLKQEWSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLYNNADGE  
FAVTHMTKAHLFSTGTVHWVPPAIYKSSCSIDVTFFPFDQQNCKMKFGSWTYDKAKIDLEQMEQTVDLKDYWESGEW  
AIVNATGTYNISKYDCCAIEYDPVTYAFVIRRLPLFYTINLIIPCLLISCLTVLVFYLPSDCGEKITLCISVLLSLT  
VFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLISIVITVFVLNVHHRSPSTHTMPHWVRGALLGCVPRWLLMNRPPP  
PVELCHPLRLKLSPSYHWLESNVDAEEREVVVEEDRWACAGHVAPSVGTLCSHGHLHSGASGPKAEALLQEGELLL  
SPHMQKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWLFIIVCFLGTIGLFLPPFLAGMI

Transmembrane domains.

amino acids 2-22, 264-284, 299-319, 330-350, 501-521

N-glycosylation sites.

amino acids 79-82, 129-132, 235-238

Tyrosine kinase phosphorylation site.

amino acids 468-475

N-myristoylation sites.

amino acids 25-30, 52-57, 89-94, 128-133, 238-243, 368-373, 434-439

Neurotransmitter-gated ion-channels signature.

amino acids 183-197

Neurotransmitter-gated ion-channel ligand binding domain.

amino acids 59-265

Neurotransmitter-gated ion-channel transmembrane domain.

amino acids 272-520

## **FIGURE 113**

MLPPGTATLLTLLLAAGSLGQKPQRPRRPASPISTIQPKANFDAQQFAGTWLLVAVGSACRFLQEQGHRAEATTLHV  
APQGTAMAVSTFRKLDGICWQVRQLYGDTGVLGRFLLQARGARGAVNVVVAETDYQSFAVLYLERAGQLSVKLYARS  
LPVSDSVLSGFEQVRVQEAHLTEDQIFYFPKYGFCEAADQFHVLDEVRR

Signal sequence.

amino acids 1-20

N-myristoylation sites.

amino acids 81-86, 118-123

Lipocalin/cytosolic fatty-acid binding protein.

amino acids 46-188

## **FIGURE 114**

MRLTVLCAVCLLPGSLALPLPQEAGGMSELQWEQAQDYLRFYLYDSETKNANSLEAKLKEMQKFFGLPITGMLNSR  
VIEIMQKPRCGVPDVAEYSLFPNSPKWTSKVVITYRIVSYTRDLPHTVDRILVSKALNMWGKEIPLHFRKVVWGTADI  
MIGFARGAHGDSYPFDGPGNTLAHAFAPGTGLGGDAHFEDEDERWTDGSSLGINFLYAATHELGHSLGMGHSSDPNAV  
MYPTYGNGDPQNFKLSQDDIKGIQKLYGKRSNSRKK

Signal sequence.

amino acids 1-17

N-myristoylation sites.

amino acids 67-72, 72-77, 173-178, 183-188, 201-206, 221-226

Amidation site.

amino acids 258-261

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 211-220

Matrixins cysteine switch.

amino acids 85-92

Matrixin.

amino acids 38-199

**FIGURE 115**

MAPPQVLAFGLLLAATATFAAAQEEVCENYKLAVNCFVNNNRQCQCTSVGAQNTVICSKLAAKCLVMKAEMNGSK  
LGRRAKPEGALQNNDGLYDPDCDESGLFKAKQCNGTSTCWCVNNTAGVRRTDKDTEITCSERVRTYWIIEELKHKARE  
KPYDSKSLRTALQKEITTRYQLDPKFITSILYENNVITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSKKM  
DLTVNGEQLDLDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVMAVVAGIVVLVISRKKRMAKYEKAEIKEMGEM  
HRELNA

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 265-285

N-glycosylation sites.

amino acids 74-77, 111-114, 198-201

Tyrosine kinase phosphorylation site.

amino acids 151-157

N-myristoylation sites.

amino acids 10-15, 52-57, 75-80, 86-91, 103-108, 112-117, 123-128, 263-268

Amidation site.

amino acids 78-81

Thyroglobulin type-1 repeat.

amino acids 66-135

**FIGURE 116**

MRQKAVSVFLCYLLLFTCSGVEAGKKKCSSESDSGSGFWKALTFMAVGGGLAVAGLPALGFTGAGIAANSVAASLMS  
WSAILNGGGVPAGGLVATLQSLGAGGSSVVIGNIGALMRYATHKYLDSEEDDEE

Signal sequence.

amino acids 1-20

Transmembrane domains.

amino acids 39-59, 90-110

Glycosaminoglycan attachment site.

amino acids 34-37

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-29

N-myristoylation sites.

amino acids 20-25, 48-53, 50-55, 63-68, 65-70, 85-90, 86-91, 90-95, 91-96, 100-105, 109-114

Amidation site.

amino acids 23-26

**FIGURE 117**

MPRAPAPLYACLLGLCALLPRLAGLNICTSGSATSCEECLLIHPKCAWCSKEDFGSPRSITSRCDLRANLVKNGCGG  
 EIESPASSFHVLRSLPLSSKSGSAGWDVIQMTPEIAVNLRPGDKTTFQLQVRQVEDYPVDLYYMDLSLSMKDDL  
 DNIRSLGTKLAEEMRKLTSNFRLGFGSFVDKDISPFSYTAPRYQTNPCIGYKLPNCVPSFGFRHLLPLTDRVDSFN  
 EEVRKQVRVSRNRDAPEGGFDAVLQAAVCKEKIGWRKDALHLLVFTTDDVPHIALDGKLGGLVQPHDGGQCHLNEANEY  
 TASNQMDYPSLALLGEKLAENNINLI FAVTKNHMYLYKNFTALIPGTTVEILDGDSKNIIQLIINAYNSIRSKVELS  
 VWDQPEDLNLFFTTATCQDGVSYPGQRKCEGLKIGDTASFEVSLEARSCPSRHEHVFAIRPVGFRDSLEVGVTYNCT  
 CGCSVGLEPNARSNGSGTYVCGLCCECPGYLGTRCECQDGENQSVYQNLCREAEGKPLCSGRGDCSCNQCSCFESE  
 FGKIYGPFCEDNFSCARNKGVLCSGHGECHCGECKCHAGYIGDNCNCSTDISTCRGRDGGICSERGHCLCGQCQCT  
 EPGAFGEMCEKCPTCPDACSTKRDCVECLLLHSGKPDNQTSLSLRDEVITWVDITVKDDQEAFLCFYKTAKDCVMM  
 FTYVELPSGKSNLTVLREPECGNTPNAMTILLAVVGSILLVGLALLAIWKLVTIHDRREFAKFQSERSRARYEMAS  
 NPLYRKPISTHTVDFTFNKFNKSYNGTVD

Signal sequence.

amino acids 1-24

Transmembrane domain.

amino acids 723-743

N-glycosylation sites.

amino acids 347-350, 460-463, 477-480, 505-508, 552-555, 586-589, 654-657, 705-708, 791-794, 795-798

Glycosaminoglycan attachment sites.

amino acids 523-526, 564-567

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 169-172

N-myristoylation sites.

amino acids 24-29, 31-36, 55-60, 98-103, 161-166, 248-253, 409-414, 415-420, 456-461, 464-469, 468-473, 480-485, 485-490, 560-565, 599-604, 611-616, 715-720

Cell attachment sequence.

amino acids 525-527

MotEGF-like domain cysteine pattern signatures.

amino acids 487-498, 574-585

Integrins beta chain cysteine-rich domain signatures.

amino acids 522-535, 563-576



## **FIGURE 118**

MLPQIPFLLLVS LNLVHGVFYAERYQMPTGIKGPLPNTKTQFFIPYTIKSKGIAVRGEQGTGPPGPAGPRGHPGPS  
GPPGKPGYGSPLQGEFGLPGPPGPSAVGKPGVPGLPGKPGERGPYGPKGDVGPAGLPGRGPPGPPGIPGPAGISV  
PGKPGQQGPTGAPGRGFPGEKGAPGVPGMNGQKGEMGYGAPGRPGERGLPGPQGPPTGSGPPGVGKRGENGVPGPQ  
GIKGRGFPGE MGPFGPPGPQGPGERGPEGIGKPGAAGAPGQPGIPGTKGLPGAPGIAGPPGPPGF GKPLPGLKG  
ERGPAGLPGGPGAKEQGPAGLP GKPLTGPPGNMGPQGPKGIPGSHGLPGPKGETGPAGPAGYPGAKGERGSPGSD  
GKPGYPGKPGLDGPKGNPGLPGPKGDPGVGGPPGLPGVPGPAGAKGMPGHNGEAGPRGAPGIPGTRGPIGPPGIPGF  
PGSKGDPGSPGPPGPAGIATKGLNGPTGPPGPPGPRGHSGEPLPGPPGPPGPPGQAVMPEGFIKAGQRPSLSGTPL  
VSANQGV TGMPVSAFTVILSKAYPAIGTPIPFDKILYNRQQHYDPRTGIFTCPGIIYYFSYHVHVKGTHVWVGLYK  
NGTPVMYTYDEYTKGYLDQASGSAIIDLTENDQVWLQLPNAESNGLYSSEYVHSSFSGFLVAPM

Signal sequence.

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 116-123

N-myristoylation sites.

amino acids 18-23, 276-281, 317-322, 350-355, 380-385, 415-420, 446-451,  
529-534, 548-553, 587-592, 613-618, 661-666

Amidation site.

amino acids 219-224

Clq domain signature.

amino acids 571-601

Clq domain.

amino acids 553-677

Collagen triple helix repeat (20 copies).

amino acids 92-150, 156-214, 223-281, 282-340, 344-403, 404-463, 464-522

**FIGURE 119**

MLLWSLLVIFDAVTEQADSLTLVAPSSVFEGDSIVLKCQGEQNWKIQKMAYHKDNKELSVFKKFSDFLIQSAVLSDS  
GNYFCSTKGQLFLWDKTSNIVKIKVQELFQRPVLTASSFQPIEGGPVSLKCETRLSPQRLDVQLQFCFFRENQVLGS  
GWSSSPELQISAVWSEDTGSYWCKAETVTHRIRKQSLQSQIHVQRIPISNVSLAIRAPGGQVTEGQKLILLCSVAGG  
TGNVTFSWYREATGTSMGKKTQRSLSAELEIPAVKESDAGKYICRADNGHVPIQSKVVNIPVRIPVSRPVLTLRSPG  
AQAAGDILLELHCEALRGSPPILYQFYHEDVTLGNSSAPSGGGASFNLSLTAEHSGNYSCEANGLGAQCSEAVPVS  
ISGPDGYRRDLMTAGVLWGLFGVLGFTGVALLLYALFHKISGESSATNEPRGASRPNPQEFTYSSPTPDMEELQPVY  
VNVGSVDVDVVYSQVWSMQQPESANIRTLLLENKDSQVIYSSVKKS

Signal sequence.

amino acids 1-14

Transmembrane domain.

amino acids 400-420

N-glycosylation sites.

amino acids 204-207, 234-237, 343-346, 355-358, 365-368

Glycosaminoglycan attachment site.

amino acids 348-351

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 62-65, 187-190

Tyrosine kinase phosphorylation site.

amino acids 266-273

N-myristoylation sites.

amino acids 78-83, 121-126, 153-158, 173-178, 213-218, 230-235, 245-250, 308-313, 349-354, 351-356, 364-369, 375-380, 400-405

Amidation site.

amino acids 248-251

Immunoglobulin domains.

amino acids 17-84, 121-179, 219-277, 314-370

## **FIGURE 120**

LRQGLSGGGGSLASGGPGPGHASLSQRLRLYLADSWNQCDLVALTCFLLGVGCRLTPGLYHLGRTVLCIDFMVFTVR  
LLHIFTVNKQLGPKIVIVSKMMKDVFFFLFLLGVWLVAYGVATEGLLRPRDSDFPSILRRVFYRPYLQIFGQIPQED  
MDVALMEHSNCSSEPGFWAHPPGAQAGTCVSQYANWLVLVLLLVIFLLVANILLVNLLIAMFSYTFGKVQGNSDLYWK  
AQRYRLIREFHSRPALAPPFIVISHLRLLLRQLCRRPRSPQPSSPALEHFRVYLSKEAERKLLTWESVHKENFLAR  
ARDKRESDSERLKRTSQKVDLALKQLGHIREYEQRLKVLEREVQQCSRVLGWVAEALSRSALLPPGGPPPPDLPGSKD

Transmembrane domains.

amino acids 34-54, 63-83, 99-119, 189-209, 238-258

N-glycosylation site.

amino acids 164-167

Glycosaminoglycan attachment site.

amino acids 6-9

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 312-315, 321-324

N-myristoylation sites.

amino acids 4-9, 7-12, 9-14, 10-15, 177-182, 181-186

Leucine zipper pattern.

amino acids 41-62

**FIGURE 121**

MGPSCPVFLSFTKLSLWLLLLTPAGGEEAKRPPPRAPGDPLSSPSPTALPQGGSHTEDETDLFKHLFRGYNRWARPV  
 PNTSDVVIVRFGLSIAQLIDVDEKNQMMTTNVWLKQEWSYKLRWNPADFGNITSLRVPSEMIWIPDIVLYNNADGE  
 FAVTHMTKAHLFSTGTVHWVPPAIYKSSCSIDVTFFPFDDQNCKMKFGSWTYDKAKIDLEQMEQTVDLKDYWESGEW  
 AIVNATGTYNSSKYDCCAIEYDPVTYAFVIRRLPLFYITINLIIPCLLISCLTVLVFYLPSDCGEKITLCISVLLSLT  
 VFLLLITEIIPSTSLVIPLIGEYLLFTMIFVTLISIVITVFVLNVHHRSPSTHTMPHWVRGALLGCVPRWLLMNRPPP  
 PVELCHPLRLKLSPSYHWLESNVDAEEREVVVEEDRWACAGHVAPSVGTLCSHGHLHSGASGPKAEALLQEGELL  
 SPHMQKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWLFIIIVCFLGTIGLFLPPFLAGMI

Signal sequence.

amino acids 1-26

Transmembrane domains.

amino acids 264-284, 299-319, 330-350, 501-521

N-glycosylation sites.

amino acids 79-82, 129-132, 235-238

Tyrosine kinase phosphorylation site.

amino acids 468-475

N-myristoylation sites.

amino acids 25-30, 52-57, 89-94, 128-133, 238-243, 368-373, 434-439

Neurotransmitter-gated ion-channel signature.

amino acids 183-197

Neurotransmitter-gated ion-channel ligand binding domain.

amino acids 59-265

Neurotransmitter-gated ion-channel transmembrane region.

amino acids 272-520

## **FIGURE 122**

MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLLHLHQTAAHAEFDCPSELQHTQELFPQWHLPIKI  
AAIIASLTFLYTLREVIHPLATSHQQYFYKIPILVINKVLPMSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWL  
DKWMLTRKQFGLLSFFFAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIVGLAILA  
LLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVVLIKFSIL  
FLPCLRKKILKIRHWEDVTKINKTEICSQL

Transmembrane domains.

amino acids 72-92, 116-136, 158-178, 218-238, 254-274, 291-311

N-glycosylation sites.

amino acids 143-146, 331-334

Tyrosine kinase phosphorylation site.

amino acids 19-27

N-myristoylation sites.

amino acids 133-138, 265-270

**FIGURE 123**

MHNTTEKPTDAYGELDFTGAGRKHSNFLRLSDRTDPAAVYSLVTRTWGFRAPNLVSVLGGSGGPVLQTLQDLLRR  
 GLVRAAQSTGAWIVTGGLHTGIGRHVGAVRDHQMASTGGTKVVAMGVAPWGVVRNRDTLINPKGSFPARYRWRGDP  
 EDGVQFPLDYNYSAFFLVDDGTHGCLGGENRFRRLRESYISQQKTGVGGTGIDIPVLLLLIDGDEKMLTRIENATQA  
 QLPCLLVAGSGGAADCLAETLEDTLAPGSGGARQGEARDRIIRFFPKGDLEVLQAQVERIMTRKELTTYSSSEDGSE  
 EFETIVLKALVKACGSSEASAYLDELRLAVAWNRVDIAQSELFRGDIQWRSFHLEASLMDALLNDRPEFVRLLI SHG  
 LSLGHFLTPMRLAQLYSAAPSNLIRNLLDQASHSAGTKAPALKGGAELRPPDVGHVLRMLLGKMCAPRYPSGGAW  
 DPHPGQGFGESMYLLSDKATSPLSLDAGLGQAPWSDLLLWALLLNRAQMAMYFWEMGSNAVSSALGACLLLRVMARL  
 EPDAEEAARRKDLAFKFEGMGVDLFGE CYRSSEVRAARLLLRCPWGDATCQLQAMQADARAFFAQDGVQSLLTQK  
 WWGDMASTTPIWALVLAFFCPPLIYTRLITFRKSEEEPTREELEFDMDSVINGEGPVGTADPAEKTPLGVPRQSGRP  
 GCCGGRCGRRCLRRWFHFWGAPVTIFMGNVVS YLLFLLLSRVLLVDFQPAPPGSLELLLYFWAFTLLCEELRQGL  
 SGGGGS LASGGPGPGHASLSQRLRLYLADSWNQCDLVALTCFLLGVGCRLTPGLYHLGRTVLCIDFMVFTVRL LHIF  
 TVNKQLGPKIVIVSKMMKDVFFFLFLLGVWLVA YGVATEGLLRPRDSDFPSILRRVFYRPLYQIFGQIPQEDMDVAL  
 MEHSNCSSEPGFWAHPPGAQAGTCVSQYANWLVLVLLVIFLLVANILLVNLLIAMFSYTFGKVQGNSDLYWKAQRYR  
 LIREFHSR PALAPPFIVISHLRLLLRQLCRRPRSPQPSSPALEHFRVYLSKEAERKLLTWESVHKENFLARARDKR  
 ESDSERLERTSQKVDLALKQLGHIREYEQRLKVLEREVQQCSRVLGWVT

Transmembrane domains.

amino acids 621-641, 713-733, 798-818, 828-848, 864-884, 954-974, 1003-1023

N-glycosylation sites.

amino acids 3-6, 165-168, 227-230, 929-932

Glycosaminoglycan attachment site.

amino acids 771-774

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 22-25, 1077-1080

N-myristoylation sites.

amino acids 78-83, 93-98, 94-99, 129-134, 142-147, 175-180, 178-183, 200-205,  
 240-245, 243-248, 259-264, 262-267, 323-328, 385-390, 467-472, 694-699, 697-702,  
 701-706, 714-719, 722-727, 769-774, 772-777, 774-779, 775-780, 942-947, 946-951

Amidation sites.

amino acids 20-23, 701-704

Cell attachment sequences.

amino acids 151-153, 352-354

Leucine zipper pattern.

amino acids 806-827

**FIGURE 124**

MHLHRRFTDLIWKNLCPALIVILGNPIHDKTITSHTSSTSTLSLESDSASPGVSDHGRSGSCSCTAPALSGPVARTI  
 YYIAAELVRLVGSVDSMKPVLSLYHRVLLYPPQHRVEAIKIMKEILGSPQRLCDLAGPSSTESERKRSISKRS  
 HLDLLKLIMDMTEACIKGGIEACYAAVSCVCTLLGALDELSQGKGLSEGQVQLLLLLRLEELKDGAWSRDSMEINE  
 ADFRWQRRVLSSEHTPWESGNERSLDISISVTDTGQTTLEGELGQTTPEHDHSGNHKNSLKSPAIEGKETLSKVLE  
 TEAVDQPDVVQSRSHTVYPYDITNFLSVDCRTRSYGSRYSSENFSDDDQDLRTEFDSCDQYSMAAEKDSGRSDVSDI  
 GSDNCSLADEEQTPRDCLGHRSLRTAALSLLKLNQEQADQHSARLFIQSLEGLLPRLLSLSNVEEVDLTALQNFSTF  
 CSGMMHSPGFDGNSLSFQMLMNADSLYTAAHCALLNLKLSHGDIYRKRPTLAPGVMKDFMKQVQTSGLVMVFSQA  
 WIEELYHQVLDRNMLGEAGYWGSPEDNSLPLITMLTDIDGLESAIGGQLMASAATESPFAQSRRIDSTVAGVAFA  
 RYILVGCWKNLIDTLSTPLTGRMAGSSKGLAFILGAEGIKEQNQKERDAICMSLDGLRKAARLSCALGVAANCASAL  
 AQMAAASCVEEKEEREAEQEPSDAITQVKLKVEQKLEQIGKVQGVWLHTAHVLCMEAILSVGLEMGSHNPDCWPHVF  
 RVCEYVGTLEHNHFDGASQPPLTISQPQKATGSAGLLGDPECEGSPPEHSPPEQGRSLSTAPVVQPLSIQDLVREGS  
 RGRASDFRGGSLMSGSSAAKVVLTLSTQADRLFEDATDKNLNLMALGGFLYQLKKASQSOLFHSVTDTVDSLAMPGE  
 VKSTQDRKSALHLFRLGNAMLRIVRSKARPLLHVMRCWSLVAPHLVEAACHKERHVSQKAVSFIHDIILTEVLTWNE  
 PPHFHFNEALFRPFERIMQLELCDEEDVQDQVVTISIGELVEVCSTQIQSGWRPLFSALETVHGGNKSEMKEYLVGDYS  
 MGKGQAPVDFVFEAFNLNTDNIQVFANAATSYIMCLMKFVKGLGEVDCKEIGDCAPAPGAPSTDLCLPALDYLRRCSQ  
 LLAKIYKMPLKPIFLSGRLAGLPRRLQEQSASSEDGIESVLSDFDDDTGLIEVWIIILEQLTAAVSNCPRQHQPPTL  
 DLLFELLRDVTKTPGPGFGIYAVVHLLLPVMSVWLRRSHKDHYSWDMASANFKHAIGLSCELVVEHIQSFLHSDIRY  
 ESMINTMLKDLFELLVACVAKPTETISRVCSCIRYVLTAGPVFTEEMWRLACCALQDAFSATLKPVKDLLGCFHS  
 GTESFSGEGCQVRVAAPSSSPSAEAYWRIRAMAQQVFMMLDTQCSPKTPNNFDHAQSCQLIELPPDEKPNGHTKKS  
 VSFREIVSVLLSHQVLLQNLIDILLEEFVKGPSPGEEKTIQVPEAKLAGFLRYISMQLAVIFDLLLLDSYRTAREFD  
 TSPGLKCLLKKVSGIGGAANLYRQSAMSFNIYFHALVCAVLTNQETITAEQVKKVLFEDDERSTDSSQQCSSEDEDI  
 FEETAQVSPPRGKEKRQWRARMPLLSVQPVSNADWVWLKRLHKLCEMELCNNYIQMHLDLENCMEEPPIFKGDPFFI  
 LPSFQSESSTPSTGGFSGKETPSEDDRSQSREHMGESLSLKAGGGDLLLPSPKVEKKDPSRKKEWWENAGNKIYTM  
 AADKTIKLMTEYKKRKQQHNLSAFPKEVKVEKKGEPLGPRGQDSPLLQRPQHLMDQGMHRSFSAGPELLRQDKRP  
 RSGSTGSSLSVSVRDAEAQIAWTNMVLTVLNQIQILPDQFTTALQPAVFPCISQLTCHVTDIRVRQAVREWLGVRG  
 RYVDIIV

Transmembrane domains.

amino acids 482-502, 1243-1263, 1510-1530

N-glycosylation sites.

amino acids 350-353, 389-392, 475-478, 1065-1068, 1792-1795

Glycosaminoglycan attachment sites.

amino acids 1392-1395, 1553-1556

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 5-8, 145-148, 151-154, 511-514, 900-903, 1151-1154, 1550-1153

Tyrosine kinase phosphorylation site.

amino acids 172-179, 1269-1276

N-myristoylation sites.

amino acids 59-64, 61-66, 89-94, 165-170, 173-178, 174-179, 200-205, 219-224,  
 251-256, 285-290, 343-348, 386-391, 579-584, 587-592, 612-617, 622-627, 641-646,  
 672-677, 684-689, 755-760, 857-862, 862-867, 1063-1068, 1136-1141, 1382-1387,  
 1554-1559, 1556-1561, 1708-1713, 1851-1856, 1854-1859

## **FIGURE 125**

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILIST  
SSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPVTKIGVAAVVRG  
AALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGLT  
REAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLF  
HVATHASEP

Transmembrane domains.

amino acids 27-47, 61-81, 99-119, 141-161, 205-225, 239-259, 273-293

N-glycosylation sites.

amino acids 7-10, 44-47, 90-93

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 268-271

N-myristoylation sites.

amino acids 6-11, 21-26, 111-116, 240-245

7 transmembrane receptor (rhodopsin family).

amino acids 43-293



**FIGURE 126**

MGSNSGQAGRHIYKSLADDGPFDSVEPPKRPTSRLLIMHSMAMFGREFCYAVEAAYVTPVLLSVGLPSSLYSIVWFLS  
PILGFLLPVVGASDHCRRSRWGRRRPYILTLGVMLVGMALYLNATVVAALIANPRRKLVAISVTMIGVVLDFD  
AADFIDGPIKAYLFDVCSHQDKEKGLHYHALFTGFGGALGYLLGAIDWAHLELGRLLGTEFQVMFFFSALVLTLCFT  
VHLCSISEAPLTEVAKGIPPQQTPODPPLSSDGMIEYGSIEKVKNGYVNPPELAMQGAKNKNHAEQTRRAMTLKSLLR  
ALVNMPPHYRYLCISHLIGWTAFLSNMLFFTDFMGQIVYRGDPYSAHNSTEFLLIYERGVEVGCWGCFCINSVFSSLYS  
YFQKVLVSYIGLKGLYFTGYLLFGLGTGFIGLFPNVYSTLVLCSLFGVMSSTLYTVFNLITEYHREEEKERQQAPG  
GDPDNSVRGKGMDCATLTCMVQLAQILVGGGLGFLVNTAGTVVVVVITASAVALIGCCFVALFVRYVD

Transmembrane domains.

amino acids 68-88, 105-125, 141-161, 182-202, 216-236, 318-338, 394-414, 422-442, 501-521

N-glycosylation site.

amino acids 356-359

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 29-32

N-myristoylation sites.

amino acids 2-7, 64-69, 190-195, 366-371, 399-404, 409-414, 416-421, 432-437, 473-478, 491-496

Amidation site.

amino acids 99-102

Cell attachment sequence.

amino acids 348-350

**FIGURE 127**

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQLQSSDFHSVSKLRVL  
 ILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSFNDFDTMPICEEAGNMSHLEILGLSGAKI  
 QKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSY  
 EMQRNLSLENAKTSVLLLNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVH  
 FRVFIYQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELfKRTIQlPHLKTlILNGNkle  
 TlSLVSCFANNTPLEHLdLSQnLLQhKNdENCsWPETVVNMNLSYNKLSDSVFRCLPKSIQILDlnnnQIQTVPKET  
 IHLMALRELNIAFNFLTDLPGCSHFSRSLSVLNIEMNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETY  
 SEVMMVGWSDSYTCEYPLNLRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCClHFDLPWYLRMLGQCTQT  
 WHRVRKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI  
 FVLSPNFVQNEWCHYEFYFAHNLfHENSdHIILILLEPIPFYCIPTRYHKLKALLEKKAYLEWPKDRRKCGLFWAN  
 LRAAINVNVLATREMYELQTfTELNEESRGSTISLMRTDCL

Transmembrane domain.

amino acids 577-597

N-glycosylation sites.

amino acids 33-36, 36-39, 140-143, 189-192, 236-239, 278-281, 330-333, 416-419,  
 427-430

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 621-624

Tyrosine kinase phosphorylation site.

amino acids 746-754

N-myristoylation sites.

amino acids 148-153, 210-215, 591-596, 765-770, 800-805

Leucine zipper patterns.

amino acids 39-60, 101-122

Nt-dnaJ domain signature.

amino acids 350-369

TIR domain.

amino acids 636-774

Leucine rich repeats.

amino acids 49-72, 73-96, 97-120, 143-166, 373-394, 398-418, 422-442, 444-466,  
 467-488, 489-512

Leucine rich repeat C-terminal domain.

amino acids 522-575

**FIGURE 128**

MTRKRITYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPPWGKYDAALRTMIPFRPK  
 PRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPLSVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLV  
 MLRFQRTRLFALLGICFCIASVLGPILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTA  
 IRFRAAVSSFAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIGYTAFIAIL  
 CYPLVFPLEVMTRMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKPFAKIIEDLRRKERKLEKCGLVQSL  
 TSITLFIIPAVATAVWVLIHTSLKLTASMAFSLASLNLRLSVFFVPIAVKGLTNSKSAVMRFKKFFLQESPVF  
 YVQTLQDPSKALVFEEATLSWQQTCPGIVNGALELERNGHASEGMRPRDALGP EEGNSLGP ELHKINLVVSKGMM  
 LGVCGNTGSGKSSLLSAILEEMHLLGSGVGVQGS LAYVPQQA WIVSGNIREN ILMGGAYDKARYLQVLHCCSLNRDL  
 ELLPFGDMTEIGERGPNLSGGQKQRISLARAVYS DRQIYLLDDPLSAVDAHVGKHI FEECIKKTLRGKTVVQVTHQL  
 QYLEFCGQVILLENGKICENGTHSELMQKKGKYAQLIQMHKEATSDMLQDTAKIAEKP KVESQALATSLEESLNGN  
 AVPEHQLTQEEEMEEGSLSWRVYHHYIQAAGGYMVSCIIFFFVVLIVFLTIFSFWWLSYWLEQSGGTNSSRESNGTM  
 ADLGN IADNPQLSFYQLVYGLNALLLICVGVCS SGIFTKVTRKASTALHNKLFNKVFRCPMSFFDTIPIGRLLNCFA  
 GDLEQLDQLLPFIFSEQFLVLSLMVIAVLLIVSVLSPYILLMGAIIMVICFIYMMFKEAIGVFKRLENYSRSPFSH  
 ILNSLQGLSSIHVYGKTEDFISQFKRLTDAQNNYLLFLSSTRWMALRLEIMTNLVT LAVALFVAFGISSTPYSFKV  
 MAVNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSC PQGWPQHGEIIFQDYHMKYRDNT  
 TVLHGINLTIRGHEVVGIVGRTGSGKSSLGMA LFRVPEPMAGRILIDGVDIC SIGLEDLRSKLSVIPQDPVLLSGTI  
 RFNLDPFDRHTDQQIWDALERTFLTKAISKFPKKLHTDVVENGGNF SVGERQLLCIARAVLRNSKIILIDEATASID  
 METDTLIQRTIREAFQGCTVLVIAHRVTTVLNCDRILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSSLR

Transmembrane domains.

amino acids 163-183, 199-219, 270-290, 300-320, 381-401, 418-438, 804-824, 858-878, 902-922, 935-955, 951-971, 990-1010, 1042-1062

N-glycosylation sites.

amino acids 11-14, 633-636, 713-716, 838-841, 844-847, 992-925, 1162-1165, 1277-1280

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 3-6, 889-892, 1026-1029

N-myristoylation sites.

amino acids 14-19, 20-25, 145-150, 170-175, 202-207, 204-209, 380-385, 440-445, 489-494, 537-542, 541-546, 544-549, 547-552, 569-574, 834-839, 836-841, 877-882, 1160-1165, 1178-1183, 1203-1208, 1275-1280, 1367-1372

ATP/GTP-binding site motif A (P-loop).

amino acids 544-551, 1175-1182

ABC transporter.

amino acids 537-708, 1168-1351

ABC transporter transmembrane region.

amino acids 163-431, 806-1095

**FIGURE 129**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGI FYLT LFLILGTCTLFFAFECRYLAVQLSPAIPVFAAMLFL  
FSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPPRIKNFQINNQIVKLKYCYTCKIFRPPRASH  
CSICDNCVERFDHHC PWVGNCVGKRNRYFYLFILSLSLLTIYVFAFNIVYVALKSLKIGFLET LKETPGTVLEVLI  
CFFTLWSVVGLTGFHTFLVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESG  
SRPPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPEPQEA AEAEK

Transmembrane domains.

amino acids 32-52, 66-86, 184-204, 227-247

N-glycosylation site.

amino acids 253-256

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 8-11

N-myristoylation sites.

amino acids 173-178, 262-267

Amidation site.

amino acids 176-179

DHHC zinc finger domain.

amino acids 130-194

**FIGURE 130**

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALVGLIGAVKHHQVLLFF  
YMIILLLVFIVQFSVSCACLALNQEQGQLLEVGNNTASARNDIQRNLNCCGFRSVNPNDTCLASCVKSDHSCSPC  
APIIGEYAGEVLRFRVGGIGLFFSFTEILGVWLTYRNRNQDPRANPSAFL

Transmembrane domains.

amino acids 10-30, 43-63, 75-95, 163-183

N-glycosylation sites.

amino acids 113-116, 137-140

N-myristoylation sites.

amino acids 4-9, 34-39, 38-43, 47-52, 63-68, 173-178, 183-188

Tetraspanin family homology.

amino acids 10-194

## **FIGURE 131**

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVKAYTFSEPFHLIVSY  
DWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGPNREFSITVVQKADSGHYHCSGIFQSPGPPI  
PETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTAS  
EDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSAAPPPTLNPA PQKSAAPGTAPEEAPGFLPPPPTPSSDPGFSS  
PLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence.

amino acids 1-17

N-myristoylation sites.

amino acids 153-158, 185-190, 236-241, 262-267, 352-357

Leucine zipper pattern.

amino acids 12-33

## **FIGURE 132**

MPGGCSRGPAAAGDGRRLRLARLALVLLGWSSSSPTSSASSFSSSAPFLASAVSAQPPLPDQCPALCECSEAARTVKC  
VNRNLTEVPTDLPAYVRNLF LTGNQLAVLPAGAFARRFPPLAELAALNLSGSRLDEV RAGAFEHLPSLRQLDLSHNPL  
ADLSPFAFSGSNASVSAPSPLVELILNHIVPPEDERQNRSFEGMVVAALLAGRALQGLRRLELASNHFLYLPRDVLA  
QLPSLRHLDLSNNSLVSLTYVSFRNLTHLESLHLEDNALKVLHNGTLAELQGLPHIRVFLDNNPWVCDCHMADMVTW  
LKETE VVQGDRLTCAYPEKMRNRVLELNSADLDCDPILPPSLQTSYVFLGIVLALIGAIFLLVLYLNRKG IKKWM  
HNIRDACRDHMEGYHYRYEINADPRLTNLSSNSDV

Signal sequence.

amino acids 1-31

Transmembrane domain.

amino acids 355-375

N-glycosylation sites.

amino acids 81-84, 124-127, 166-169, 192-195, 243-246, 256-259, 275-278, 413-416

Tyrosine kinase phosphorylation site.

amino acids 393-401

N-myristoylation sites.

amino acids 100-105, 164-169, 197-199, 360-365

Leucine zipper pattern.

amino acids 82-103

Leucine rich repeats.

amino acids 92-115, 119-142, 143-166, 211-234, 235-258, 259-282

Leucine rich repeat C-terminal domain.

amino acids 294-345

Leucine rich repeat N-terminal domain.

amino acids 61-90

## **FIGURE 133**

MAPPQVLAFGLLLAATATFAAAQEEVCENYKLAVNCFVNNNRQCQCTSVGAQNTVICSKLAAKCLVMKAEMNGSK  
LGRRAKPEGALQNNNDGLYDPDCDESGLFKAKQCNGTSTCWCVNNTAGVRRTDKDTTEITCSERVRTYWIIIELKHKARE  
KPYDSKSLRTALQKEITTRYQLDPKFITSILYENNVITIDLVQNSSQKTQNDVDIADVAYYFEKDVKGESLFHSSKM  
DLTVNGEQLDLDPGQTLIYYVDEKAPEFSMQGLKAGVIAVIVVVVIAVVAGIVVLVISRKKRMAKYEKAEIKEMGEM  
HRELNA

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 265-285

N-glycosylation sites.

amino acids 74-77, 111-114, 198-201

Tyrosine kinase phosphorylation site.

amino acids 151-157

N-myristoylation sites.

amino acids 10-15, 52-57, 75-80, 86-91, 103-108, 112-117, 123-128, 263-268

Amidation site.

amino acids 78-81

Thyroglobulin type-1 repeat.

amino acids 66-135



**FIGURE 134A**

MPCGFSPSPVAHHLVPGPPDTPAQQLRCGWTVGGWLLSLVRGLLPCLPPGARTAEGPIMVLAVSLLLPSLTLL  
VSHLSSSQDVSSEPSSEQQLCALSKHPTVAFEDLQPWVSNTYPGARDFSQLALDPSGNQLIVGARNYLFRLSLANV  
SLLQATEWASSEDTRRSCQSKGKTEEECONYVRVLIVAGRKVFMCGTNAFSPMCTSRQVGNLSRTIEKINGVARCPY  
DPRHNSTAVISSQGELYAATVIDFSGRDPAIYRSLGSGPPLRTAQYNSKWLNEPNFVAAAYDIGLFAYFFLRNAVEH  
DCGRTVYSRVARVCKNDVGGRFLEDWTTFMKARLNC SRPGEVPFYYNELQSAFHLPEQDLIYGVFTTNVNSIAAS  
AVCAFNLSAISQAFNGPFRYQENPRAAWLPPIANPIPNFQCGTLPETGPNENLTERSLQDAQRLFLMSEAVQPVTPEP  
CVTQDSVRFSHLVVDLVQAKDTLYHVLVYIGTESGTILKALSTASRSLHGCYLEELHVLPPGRREPLRSLRILHSARA  
LFVGLRDGVLRVPLERCAAYRSQGACLGARDPYCGWDGKQQRCSSTLEDSSNMSLWTQNTACPVNRNVTRDGGFGPWS  
PWQPCHELDGDNSSGSLCRARSCDSPRPRCGGLDCLGPAIHIANCSRNGAWTPWSSWALCSTSCGIGFQVRQRSCSN  
PAPRHGGRI FVGKSREERFCNENTPCPVPIFWASWGSWSKCSSNCGGGMQSRRRACENGNSCLGCGEFKTCNPEGCP  
EVRNTPWTPWLPVNVTOGGARQEQRFRTCRAPLADPHGLQFGRRTETRTCPADGSGSCDTDALVEVLLRSGSTS  
PHTVSGGWAAGWPWSSCSRDCELGFRVRKRTCTNPEPRNGGLPCVGDAAEYQDCNPQACPVRGAWSCWTSWSPCSAS  
CGGGHYQRTSRCTSPAPSPGEDI CLGLHTEEALCATQACPGWSPWSEWSKCTDDGAQSRSRHCELLPGSSACAGNS  
SQSRPCPYSEIPVILPASSMEEATDCAGKRNRTYLMRSSQPSSTPLQSLDSFHILLQTAKLCWGPCHCFEMGSISST  
WWPRASPASWALGS

Signal sequence.

amino acids 1-42

Transmembrane domain.

amino acids 60-80

N-glycosylation sites.

amino acids 117-120, 153-156, 215-218, 236-239, 345-348, 391-394, 436-439, 590-593, 597-600, 605-608, 660-663, 785-788, 1000-1003, 1032-1035

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 773-776, 815-818, 875-878

Tyrosine kinase phosphorylation sites.

amino acids 177-185, 348-356

N-myristoylation sites.

amino acids 42-47, 50-55, 373-378, 492-497, 543-548, 563-568, 630-635, 647-652, 740-745, 810-815, 827-832, 829-834, 853-858, 887-892, 910-915, 993-998, 1073-1078

Amidation sites.

amino acids 192-195, 522-525, 813-816, 1028-1031

ATP/GTP-binding site motif A (P-loop).

amino acids 700-707

Cytochrome c oxidase subunit II, copper A binding region signature.

amino acids 921-929

Growth factor and cytokines receptors family signature 2.

amino acids 967-973

Sema domain.

amino acids 126-537

**FIGURE 134B**

Thrombospondin type 1 domains.

amino acids 613-661, 668-719, 726-769, 856-906, 913-963, 967-1007

Plexin repeat.

amino acids 555-602

Plant PEC family metallothionein.

amino acids 712-791

## **FIGURE 135**

MAKDNSTVRCFQGLLIFGNVIIGCCGIALTAECIFFVSDQHSLYPLLEATDNDDIYGAAWIGIFVGICLFCLSVLGI  
VGIMKSSRKILLAYFILMFIVYAFEVASCITAATQQDFFT PNLFLKQMLERYQNNSPPNDDQWKNNGVTKTWDRM  
LQDNCCGVNGPSDWQKYTSAFR TENNDADYPWPRQCCVMNNLKEPLNLEACKLGVPGFYHNQGCYELISGPMNRHAW  
GVAWFGFAILCWTFWVLLGTMFYWSRIEY

Transmembrane domains.

amino acids 12-32, 54-74, 89-109, 231-251

N-glycosylation site.

amino acids 5-8

N-myristoylation sites.

amino acids 26-31, 62-67, 79-84, 145-150

Tetraspanin family homology.

amino acids 12-258

## **FIGURE 136**

MFDKTRLPYVALDVLCVLLAGLPFAIFTSRHITSRHTPFQRGVFCNDESIKYPYKEDTIPYALLGGIIPFSIIVII  
LGETLSVYCNLLHSNSFIRNNYIATIIYKAIGTFLFGAAASQSLTDIAKYSIGRLRPHFLDVCDPDWSKINCSDGYIE  
YYICRGNAERVKEGRLSFYSGHSSFSMYCMLFVALYLQARMKGDWARLLRPTLQFGLVAVSIYVGLSRVSDYKHHWS  
DVLTLGLIQGALVAILVAVYVSDFFKERTSFKERKEEDSHTTLHETPTTGNHYPSNHQP

Transmembrane domains.

amino acids 7-27, 61-81, 97-117, 172-192, 200-220, 233-253

N-glycosylation site.

amino acids 147-150

N-myristoylation sites.

amino acids 21-26, 42-47, 113-118, 236-241, 240-245

PAP2 superfamily.

amino acids 105-256

**FIGURE 137**

MLLWLLLLILTPGREQSGVAPKAVLLLNPPWSTAFKGEKVALICSSISHSLAQGDTYWYHDEKLLKIKHDKIQITEP  
 GNYQCKTRGSSSLSDAVHVEFSPDWLILQALHPVFEGDNVILRCQGKDNKNTHQKVYYKDQKQLPNSYNLEKITVNSV  
 SRDNSKYHCTAYRKFYILDIEVTSKPLNIQVQELFLHPVLRASSSTPIEGSPMTLTCETQLSPQRPDVQLQFSLFRD  
 SQTGLGLGWSRSPRLQIPAMWTEDSGSYWCEVETVTHSIKKRSLRSQIRVQRPVPSNVNLEIRPTGGQLIEGENMVLII  
 CSVAQSGSTVTFSWHKEGRVRSLSGRKTQRSLLAELHVLTVKESDAGRYYCAADNVHSPILSTWIRVTVRIPVSHPV  
 TFRAPRAHTVVGDLLELHCESLRGSPPILYRFYHEDVTLGNSSAPSGGGASFNLSTAEHSGNYSCDADNGLGAQHS  
 HGVSLRVTVPVSRLVTLRAPGAQAVVGDLLELHCESLRGSPPILYWYFHHEDDTLGNISAHSGGGASFNLSTTEHS  
 GNYSCDADNGLGAQHSKVVTLNVTGTSRNRGTAAAGITGLVLSILVLAALLHYARARRKPGGLSATGTSSHS  
 SECQEPSSSRPSRIDPQEPHSTKPLAPMELEPMYSNVNPGDSNPIYSQIWSIQHTKENSANCPMMHQEHEELTVLYS  
 ELKKTHPDDSAGEASSRGRAHEEDDEENYENVPRVLLASDH

Signal sequence.

amino acids 1-13

Transmembrane domain.

amino acids 574-594

N-glycosylation sites.

amino acids 426-429, 438-441, 448-451, 519-522, 531-534, 541-544, 561-561, 568-571

Glycosaminoglycan attachment sites.

amino acids 431-434, 524-527

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-273

Tyrosine kinase phosphorylation site.

amino acids 349-356

N-myristoylation sites.

amino acids 78-83, 86-91, 204-209, 236-241, 256-261, 432-437, 434-439, 447-452, 458-463, 518-523, 525-530, 527-532, 540-545, 551-556, 564-569, 571-576, 579-584, 604-609, 605-610

Amidation site.

amino acids 331-334

N-6 Adenine-specific DNA methylases signature.

amino acids 25-31

Immunoglobulin domains.

amino acids 37-84, 113-165, 204-262, 302-360, 397-453, 490-546

**FIGURE 138**

MEGGAAAATPTALPYYVAFS~~Q~~LLGLTLVAMTGAWLGLYRGGIAWESDLQFNAHPLCMVIGLIFLQGNALLVYRVFRN  
EAKRTTKVLHGLLHIFALVIALVGLVAVFDYHRKKGYADLYSLHSWCGILVFVLYFVQWLVGFSFFLFPGASFSLRS  
RYRPQHIFFGATIFLLPVGTALLGLKEALLFNLGGKYS~~A~~FEPEGVLANVLG~~L~~LLACFGGAVLYILTRADWKRPSQAE  
EQALSMDFKTLRQGDSPGSQ

Transmembrane domains.

amino acids 13-33, 51-71, 85-105, 123-143, 161-181, 198-218

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 80-83, 225-228

N-myristoylation sites.

amino acids 3-8, 4-9, 32-37, 36-41, 147-152, 178-183, 188-193, 198-203, 205-210

Cytochrome b561 homology.

amino acids 1-238

## **FIGURE 139**

MRQLCRGRVLGISVAIAHGVFSGSLNILLKFLISRYQFSFLTTLVQCLTSSTAALSLELLRRLGLIAVPPFGLSLARS  
FAGVAVLSTLQSSLTLWSLRGLSLPMYVVFKRCLPLVTMLIGVLVLKNGAPSPGVLA AVLITTCGAALAGAGDLTGD  
PIGYVTGVLAVLVHAAVLVLIQKASADTEHGPLTAQYVIAVSATPLLVICFASTDSIHAWTFPGWKDPAMVCIFVA  
CILIGCAMNFTTLHCTYINSVTTSLFIAGVVVNTLGSIIYCVAKFMETRKQSNYEDLEAQPRGEEAQLSGDQLPFV  
MEELPGEGGNRSEGGEAAGGPAQESRQEVGRSPRGVPLVAGSSEEGSRRSLKDAYLEVWRLVRGTRYMKKDYLIEN  
EELPSP

Transmembrane domains.

amino acids 8-28, 51-71, 103-123, 119-139, 153-173, 189-209, 221-241, 253-273

N-glycosylation site.

amino acids 240-243

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 281-284

N-myristoylation sites.

amino acids 11-16, 19-24, 71-76, 131-136, 142-147, 236-241, 261-266, 317-322,  
323-328, 340-345, 355-360

**FIGURE 140**

MARLALSPVPSHWMVALLLLSAEPVPAARSEDYRNPKGSAQSRIWQSPRFIARKRGFTVKMH CYMNSASGNVSWL  
WKQEMDENPQQLKLEKGRMEESQNESLATLTIQGIRFEDNGIYFCQQKCNNTSEVYQGCGETLRVMGFSTLAQLKQR  
NTLKDGIIMIQTLLIILFIIIVPIFLLLDKDDSKAGMEEDHTYEGLDIDQTATYEDIVTLRTGEVKWSVGEHPGQE

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 159-179

N-glycosylation sites.

amino acids 73-76, 101-104, 127-130, 128-131

Tyrosine kinase phosphorylation site.

amino acids 113-120

N-myristoylation sites.

amino acids 40-45, 118-123

Immunoglobulin domain.

amino acids 58-124

Immunoreceptor tyrosine-based activation motif.

amino acids 193-213



**FIGURE 141**

MGLPEPGPLRLALLLLLLLLLLLLLLLRLQHLAAAAADPLLGGQGPAAKECEKDQFQCRNERCIPSVWRCEDDDDCLDHSD  
 EDDCPKKTCADSDFTCDNHGCIHERWKCDGEEECPDGSDESEATCTKQVCPAEKLSCGPTSHKCVPASWRCDGEKDC  
 EGGADEAGCATSLGTCRGDEFQCGDGTCLVLAIKHCNQEQDCPDGSDEAGCLQGLNECLHNNGGCSHICTDLKIGFEC  
 TCPAGFQLLDQKTCGDIDECKDPDACSQICVNYKGYFKCECYPGCEMDLLTKNCKAAAGKSPSLIFTNRTSAEDRPV  
 KRNYSLIPMLKNVVALDVEVATNRIYWCDLSYRKIYSAYMDKASDPKEREVLIDEQLHSPEGLAVDWVHKHIYWTD  
 SGNKTISVATVDGRRRTLFSRNLSEPRAIADVPLRGFMYSWDWGDQAKIEKSGLNGVDRQTLVSDNIEWPNGITLD  
 LLSQRLYWVDSKLHQLSSIDFSGGNRKTLISSTDFLSHPFGIAVFEDKVFWDLENEAIFSANRLNGLEISILAENL  
 NNPHDIVIFHELKQPRAPDACELSVQPNGGCEYLCLPAPQISSHSPKYTCACPDTMWLGPDMDKRCYRDANEDSKMGS  
 TVTAAVIGIIVPIVVIALLCMSGYLIWRNWKRKNTKSMNFDNPVYRKTEEEDEDELHIGRTAQIGHVYPARVALSL  
 EDDGLP

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 619-639

N-glycosylation sites.

amino acids 299-302, 311-314, 388-391, 408-411

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 400-403, 648-651, 662-665

N-myristoylation sites.

amino acids 40-45, 114-119, 157-162, 162-167, 168-173, 198-203, 203-208, 207-212, 486-491, 529-534, 615-620

Amidation site.

amino acids 398-401

Aspartic acid and asparagine hydroxylation sites.

amino acids 222-233, 261-272

Cell attachment sequence.

amino acids 171-173

Low-density lipoprotein receptor repeats.

amino acids 332-377, 379-420, 422-464, 466-509, 510-550

Low-density lipoprotein receptor domains.

amino acids 45-83, 84-124, 125-165, 168-206

**FIGURE 142**

MPPLWALLALGCLRFGSAVNLQPQLASVTTFATNNPTLTTVALEKPLCMFDSKEALTGTHEVYLYVLVDSAISRNASV  
QDSTNTPLGSTFLQTEGGRTGPYKAVAFDLIPCSDLPSLDAIGDVSKASQILNAYLVRVGANGTCLWDPNFQGLCNA  
PLSAATEYRFKYVLVNMSTGLVEDQTLWSDPIRTNQLTPYSTIDTWPGRRSGGMIVITSILGSLPFFLLVGFAGAIA  
LSLVDMGSSDGETTHDSQITQEAVPKSLGASESSYTSVNRGPPLDRAEVYSSKLQD

Signal sequence.

amino acids 1-18

Transmembrane domain.

amino acids 211-231

N-glycosylation sites.

amino acids 74-77, 139-142, 170-173

N-myristoylation sites.

amino acids 16-21, 137-142, 238-243, 260-265

Amidation site.

amino acids 201-204

**FIGURE 143**

MRKLIAGLIFLKFWTYTVRASTDLPQTENCFQYIHQVTEISSTLPVALLRDEVPGWFLKVPEPQLISKELIMLTEVM  
EVWHGLVIAVVSIFLQACFLTAINYLLSRHMAHKSEQILKAASLQVPRPSPGHHHPFAVKEMKETQTERDIPMSDSL  
YRHSDTFPSDSLSSCSSPPACQATEDVDYDTQVVFSDPGELK

Signal sequence.

amino acids 1-20

Transmembrane domain.

amino acids 75-95

N-myristoylation site.

amino acids 82-87

Leucine zipper pattern.

amino acids 83-104

**FIGURE 144**

MAGTVRTACLVVAMLLSLDFPGQAQPPPPPPDATCHQVRSFFQRLQPGLKWVPETPVPGSDLQVCLPKGPTCCSRKM  
EEKYQLTARLNMEQLLQSASMELKFLIIQNAAVFQEAFAEIVVRHAKNYTNAMFKNNYPSLTPQAFEFVGEFFTDVSL  
YILGSDINVDDMVNELFDSLFPVIYTQLMNPGLPDSALDINECLRGARRDLKVFGNFPKLIMTQVSKSLQVTRIFLQ  
ALNLGIEVINTTDHLKFSKDCGRMLTRMWYCSYCQGLMMVKPCGGYCNVVMQGCMAGVVEIDKYWREYILSLEELVN  
GMYRIYDMENVLLGLFSTIHDSIQYVQKNAGKLTTTIGKLCAHSQQRQYRSAYYPEDLFIDKKVLKVAHVEHEETLS  
SRRRELIQKLKSFISFYALPGYICSHSPVAENDTLCWNGQELMERYSQKAARNGMKNQFNLHELKMKGPEPVVSI  
IDKLKHINQLLRTMSMPKGRVLDKNLDEEGFESGDCGDDDECIGSGDGMKVKQNQLRFLAELAYDLDDVDDAPGNS  
QQATPKDNEISTFHNLGNVHSPLKLLTSMAISVVCFFFLVH

Signal sequence.

amino acids 1-24

Transmembrane domain.

amino acids 559-579

N-glycosylation sites.

amino acids 124-127, 241-244, 418-421

Glycosaminoglycan attachment site.

amino acids 509-512

Tyrosine kinase phosphorylation sites.

amino acids 75-81, 521-528

N-myristoylation sites.

amino acids 3-8, 158-163, 186-191, 275-280, 284-289, 322-327, 508-513

Glypican homology.

amino acids 4-578

**FIGURE 145**

MGLPRGPLASLLLLQVCWLQCAASEPCRAVFREA EVTLEAGGAEQEPGQALGKVFMGCPGQEPALFSTDND DFTVRN  
 GETVQERRSLKERNPLKIFPSKRILRRHKRDWV VAPISVPENGKGFPQRLNQLKSNKDRDTKIFYSITGPGADSP P  
 EGVFAVEKETGWLLLNKPLDREEIAKYELFGH AVSENGASVEDPMNISIIIVTDQNDHKPKFTQDTFRGSVLEGLPG  
 TSVMQVTATDEDDAIYTYNGVVAYSISHSQEPKDPHLMFTIHRSTGTISVISSGLDREKVPEYTLTIQATMDGDGGS  
 TTTAVAVVEILDANDNAPMFDPOKYEAHV PENAVGHEVQRLTVTDLDAPNSPAWRATY LIMGGDDGDHFTITTHPES  
 NQGILTTRKGLDFEAKNQHTLYVEVTNEAPFVLKLPTSTATIVVHVEDVNEAPVFVPPSKVVEVQEGIPTGEPVCVY  
 TAEDPDKENQKISYRILRDPAGWLAMPDPSGQVTAVGTL DREDEQFVRNNIYEVMLAMDNGSPPTTGTGTL LLLTLI  
 DVNDHGPVPEPRQITICNQSPVRHVLNITDKDLS PHTSPFQAQLTDDSDIYWTAEVNEEGDTVVL SLKKFLKQDTYD  
 VHLSLDHGNKEQLTVIRATVCDCHGHVETCPGPWKGGFILPVLGAVLALLFLLLVL LLLVRKKRKIKEPLLLPEDD  
 TRDNVFYYGEEGGGEEDQDYDITQLHRGLEARPEV VLRNDVAPTIIPTPMYRPRPANPDEIGNFIIENLKAANTDPT  
 APPYDTLLVFDYEGSGSDAASLSSLTSSASDQDQDYDYLNEWGSRFKKLADMYGGGEDD

Signal sequence.

amino acids 1-24

Transmembrane domain.

amino acids 655-675

N-glycosylation sites.

amino acids 200-203, 566-569

N-myristoylation sites.

amino acids 48-53, 60-65, 227-232, 307-312, 370-375, 388-393, 452-457, 493-498,  
 524-529, 661-666, 786-791

Cadherins extracellular repeated domain signature.

amino acids 203-213, 316-326, 536-546

Cadherin domains.

amino acids 122-206, 220-319, 333-432, 445-539, 551-638

Cadherin cytoplasmic region.

amino acids 678-826

## **FIGURE 146**

GDCGDRGTARGTRREGTGIRSSGRAMDGNNDVTLFAPLLRDNYTLAPNASSLGPGTDLALAPASSAGPGPGLSLGP  
GPSFGFSPGPTPTPEPTTSGLAGGAASHGPSFPFPRWAPHALPFWDTPLNHGLNVFVGAALCITMLGLGCTVDVNH  
GAHVRRPVGALLAALCQFGLLPLLAFLLALAFKLDEVA AVAVLLCGCCPGGNLSNLSLLVDGDMNLSIIMTISSTL  
LALVLMPLCLWIYSWAWINTPIVQLPLGTVTTLTLCSTLIPIGLGVFIRYKYSRVADYIVKVSLSLLVTLVVLVLFIM  
TGTM LGPELLASIPAAVYVIAIFMPLAGYASGYGLATLFHLPNCKRTVCLETGSQNVQLCTAILKLAFPPQFIGSM  
YMFPLLYALFQSAEAGIFVLIYKMYGSEMLHKRDPLDEDEDTDISYKKLKEEEMADTSYGTVKAENIIMMETAQTS

Transmembrane domains.

amino acids 126-146, 161-181, 177-197, 218-238, 254-274, 289-309, 326-346

N-glycosylation sites.

amino acids 31-34, 43-46, 49-52, 206-209, 220-223

Glycosaminoglycan attachment site.

amino acids 339-342

N-myristoylation sites.

amino acids 7-12, 18-23, 56-61, 97-102, 100-105, 135-140, 144-149, 163-168, 200-205, 204-209, 205-210, 445-450

Sodium Bile acid symporter family homology.

amino acids 135-316

**FIGURE 147**

MVRRDRLRRMREWWVQVGLLAVPLLAAYLHIPPQLSPALHSWKSSGKFFTYKGLRIFYQDSVGVVGSPEIVVLLHG  
FPTSSYDWYKIWKGLTLRFHRVIALDFLGFGFSDKPRPHHYSIFEQASIVEALLRHLGLQNRRLNLLSHDYGDIVAQ  
ELLYRYKQNRSGRHTIKSLCLSNGGIFPETHRPLLQKLLKDGGVLSPILTRLMNFFVFSRGLTPVFGPYTRPSESE  
LWDMWAGIRNNDGNLVIDSLLQYINQRKKFRRRWVGALASVTIPIHFIYGPLDPVNPYPEFLELYRKTLPRSTVSIL  
DDHISHYPQLEDPMGFLNAYMGFINSF

Transmembrane domains.

amino acids 12-32, 59-79

N-glycosylation site.

amino acids 163-166

N-myristoylation sites.

amino acids 238-243, 267-272

alpha/beta hydrolase fold.

amino acids 97-332

**FIGURE 148**

GWTSHLNCGESNRPPKERSCFRVCWDHSDLFQWEVSDWHHCVLVPYARGEVKPRTAECVTAQHGLQHRMVRCIQKL  
 NRTVVANEICEHFALQPPTAQACLI PCPRDCVVSEFLPWSNCSKGCCKKLQHRTRAVIAPPLFGGLQCPNLTESRAC  
 DAPISCPLEGEEYTFSLKVGWPSKCRPLHKEINPSGRVTFLDFNSDSNERVTFKHQSYKAHHHSKSWAIEIGYQTRQ  
 VSCTRSDGQNAMLSLCLQDSFPLTVQSCIMPKDCETSQWSSWSPCSKTCRSGSLLPGFRSRNRNVKMAIGGGKECP  
 ELLEKEACIVEGELLQQCPRYSWRTSEWKECQVSLLEQQDPHWHVTGPVCGGGIQTREYCAQSVAAAAALRAKEV  
 SRPVEKALCVGPAPLPSQLCNIPCSTD CIVSSWSAWGLCIHENCHEPQGGKGFRTQRHVLMESTGPAGHCPHLVES  
 VPCEDPMC YRWLASEGICFPDHGKCGLGHRLKAVCQNDRGEDVSGSLCPVPPPPERKSCEIPCRMDCVLSEWTEWS  
 SCSQSCSNKNSDGKQTRSRTILALAGEGGKPCPPSQALQEHLNCDHSCMLHWETSPWGPCEDTLVTALNATIGW  
 NGEATCGVGIQTRRVFCVKSHVGQVMTKRCPDSTRPETVRPCFLPCKKDCIVTAFSEWTPCPRMCQAGNATVKQSR  
 RIIIEAANGGQECPD TLYEERECEDVSLCPVYRWKPQKWSPCILVPESVWQGITGSSEACGKGLQTRAVSCISDDN  
 RSAEMMECLKQTNGMPLLVQECTVPCREDCTFTAWSKFTPCSTNCEATKSRRRQLTGKSRKKEKCQDSDLPLVETE  
 LCPCDEFISQPYGNWSDCILPEGRREPHRGLRVQADSKECGEGLRFRAVACSDKNGRPVDPSEFCSSSGYIQEKC  
 VPCFDCKLSDWSSWGSCSSSCGIGVIRSKWLKEKPYNGGRPCPKLDLKNQAQVHEAVPCYSECNQYSWVVEHWSSCK  
 INNELRSLRCGGGTQSRKIRCNTADGEGGAVDSNLNQNDEIPPETQSCSLMCPNECVMSEWGLWSKCPQSCDPHTM  
 QRRTRHLLRPSLNSRTCAEDSQVQPCLLNENCFQFQYNLTWSTCQLSENAPCGQGVRTRLLSCVSDGKPKVSMQDQ  
 EQHNLEKPPQRMSIPCLVECVVNCQLSGWTAWTECSQTCGHGGRMSRTRFIIMPTQGEGRPCPTELTQEKTCPTVTPCY  
 SWVLGNWSACKLEGGDCGEGVQIRSLSCMVHSGSISHAAGRVEDALCGEMPFQDSILKQLCSVPCPGDCHLTEWSEW  
 STCELT CIDGRSFETVGRQSRRTFIIQSFENQDSCPPQVLETRPCTGGKCYHYTWKASLWNNNERTVWCQRSDGVN  
 VTGGCSPQARPAAIRQCIPACRKPF SYCTQGGVCGCEKGYTEIMRSNGFLDYCMKVP GSEDKKADVKNLSGKNRPVN  
 SKIHDIFKGSWLSQPLDPDGRVKI WVYGVSGGAFLIMIFLIFTSYLVCKKPKPHQSTPPQKPLTLAYDGDLDNM

Transmembrane domain.

amino acids 1486-1506

N-glycosylation sites.

amino acids 78-81, 118-121, 147-150, 611-614, 685-688, 770-773, 861-864, 1116-1119, 1238-1241, 1386-1389, 1454-1457

Tyrosine kinase phosphorylation sites.

amino acids 834-841, 953-960

N-myristoylation sites.

amino acids 361-366, 639-644, 746-751, 749-754, 938-943, 1013-1018, 1031-1036, 1196-1201, 1237-1242, 1246-1251, 1384-1389, 1417-1422, 1418-1423, 1421-1426, 1490-1495

Amidation sites.

amino acids 123-126, 433-436, 869-872

Growth factor and cytokines receptors family signature 2.

amino acids 268-274, 1061-1067, 1304-1310

Thrombospondin type 1 domains.

amino acids 111-160, 268-326, 416-470, 533-588, 593-658, 669-723, 803-851, 932-983, 1061-1110, 1181-1231, 1304-1360



## **FIGURE 149**

EKPVRKQTPPTTQIHCGPPKPVLSPSFKTPATPLGLSTSTGHMLMPLCGLLWWWCCCSGWYCYGLCAPAPQMLRHQ  
 GLLKCRCRMLFNDLKVFLLRRPPQAPLPMHGDPQPPGLAANNTLPALGAGGWAGWRGPREVVGREPPVPVPPPLPP  
 SSVEDDWGGPATEPPASLLSSASSDDFCKEKTEDRYSLGSSLDSGMRTPLCRICFQGPEQGELLSPCRCDGSVKCTH  
 QPCLIKWISERGCWSCELCYYKYHVIAISTKNPLQWQAISLTVIEKVQVAAAILGSLFLIASISWLIWSTFSPSARW  
 QRQDLLFQICYGMYGFMDVVCIGLIIHEGPSVYRIFKRWQAVNQWQVNLNDKTKDLEDQKAGGRTNPRTSSSTQAN  
 IPSSEETAGTPAPEQGPAQAAGHPSGPLSHHHCAYTILHILSHLRPHEQRSPPGSSRELVMRVTTVN

Transmembrane domains.

amino acids 275-295, 316-336

N-glycosylation site.

amino acids 118-121

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 5-8

Tyrosine kinase phosphorylation site.

amino acids 183-190

N-myristoylation sites.

amino acids 35-40, 78-83, 114-119, 127-132, 162-167, 225-230, 243-248

**FIGURE 150**

QEQGDKMMEEYSLEKNERACIDFAISAKPLTRHMPQNKQSFQYRMWQFVVSPPFEYTIMAMIALNTIVLMMKFYGAS  
 VAYENALRVFNIVFTSLFSLECVLKVMAFGILNYFRDAWNIFDFVTVLGSITDILVTEFGNNFINLSFLRLFRAARL  
 IKLLRQGYTIRILLWTFVQSFKALPYVCLLIAMLFFIYAIIGMQVFGNIGIDVEDEDSDEDEFQITEHNNFRTFFQA  
 LMLLFRSATGEAWHNIMLSCLSGKPCDKNSGILTRECNEFAYFYFVSFIFLCSFLMLNLFVAVIMDNFEYLTRDSS  
 ILGPHHLDEYVRVWAEYDPAACGRIHYKDMYSLLRVISPPGLGKKCPHRVACKRLLRMDLPVADDNTVHFNSTLMA  
 LIRTALDIKIAKGGADKQQMDAELRKEMMAIWPNLSQKTLDLLVTPHKSTDLTVGKIYAAMMIMEYYRQSKAKKLQA  
 MREEQDRTPLMFORMEPPSPTQEGGPGQNALPSTQLDPGGALMAHESGLKESPSWVTQRAQEMFQKTGTWSPEQGPP  
 TDM PNSQPSQSVMREMGRDGYSDSEHYLPMEGQGGAASMPRLPAENQTISDTSPMKRSASVLGPKARRLDDYSLE  
 RVPPEENQRHHQRRDRSHRASERSLGRYTDVDTGLGTDLSMTTQSGDLPSKERDQERGRPKDRKHRQH HHHHHHHH  
 HPPPPDKDRYAQERPDHGRARARDQRWSRSPSEGREHMAHRQGSSSVSGSPAPSTSGTSTPRRGRRQLPQTPSTPRP  
 HVSYSPIRKAGGSGPPQOQQOQQOQQOQAVARPGRAATSGPRRYPGPTAEPLAGDRPPTGGHSSGRSPRMERRVPG  
 PARSESPRACRHGGARWPASGPHVSEGPPGPRHHGYRGSYDEADGPGSGGGGEEAMAGAYDAPPPVRHASSGATGR  
 SPRTPRASGPACASPSRHGRRLPNGYYPAHGLARPRGPGSRKGLHEPYSESDDDWCN

Transmembrane domains.

amino acids 49-69, 86-106, 114-134, 131-151, 167-187, 183-203, 222-242, 274-294

N-glycosylation sites.

amino acids 142-145, 380-383, 419-422, 587-590

Glycosaminoglycan attachment site.

amino acids 897-900

N-myristoylation sites.

amino acids 75-80, 269-274, 502-507, 573-578, 653-658, 831-836, 896-901, 899-904, 963-968

Amidation sites.

amino acids 351-354, 756-759, 942-945

Ion transport protein homology.

amino acids 83-296

**FIGURE 151**

MRPVALLLLPSLLALLAHGLSLEAPTVGKGQAPGIEETDGELTAAPTPEQPERGVHFVTTAPTCLKLLNHHPLLEEFLL  
 HEGLEKGDDEELRPALSFQPDPPAPFTPSPLPRLANQDSRPVFTSPTPAMAAVPTQPQSKEGPWSPDPESESPMLRIT  
 APLPPGPSMAVPTLGPGEIASTTPPSRAWPTQEGPGDMGRPWWAEVVSQGAGIGIQGTITSSTASGDDEETTTTTT  
 IITTTITTVQTPGPCSWNFSGPEGSLSPTDLSSPTDVGLDCFFYISVYPGYGVEIKVKNISLREGETVTVTEGLGGP  
 DPLPLANQSFLLRGQVIRSPTHQAALRFQSLPPPAGPGTFHFHYQAYLLSCHFPRRPAYGDVTVTSLHPGGSARFHC  
 ATGYQLKGARHLTCLNATQPFWDSKEPVCIGECPGVIRNATTGRIVSPGFPGNYSNNLTCHWLLEAPEGQRLHLHFE  
 KVSLAEDDDRLLIIRNGDNVEAPPVYDSYEVEYLPPIEGLLSSGKHFFVELSTDSSGAAAGMALRYEAFQQGHCEPFV  
 KYGNFSSSTPTYVPGTTVEFSCDPGYTLEQGSIIIECVDPHDPQWNETEPACRAVCSGEITDSAGVVLSPNWPEPYG  
 RGQDCIWGVHVEEDKRIMLDIRVLRIGPGDVLTIFYDGGDLTARVLGQYSGPRSHFKLFTSMADVTIQFQSDPGTSVL  
 GYQQGFVIHFFEVPRNDTCPELPEIPNGWKSPSQPELVHGTVVITYQCYPGYQVVGSSVLMCQWDLTWSEDLPSQQRV  
 TSCHDPGDVEHSRRLISSPKFPVGATVQYICDQGFVLMGSSILTCHDRQAGSPKWSRAPKCLLEQLKPCHGLSAPE  
 NGARSPEKQLHPAGATIHFSCAPGYVLKGQASIKCVPGHPSHWSDDPPICRAASLDGSTTVAAWMVAKAPAASSTLD  
 AAHIAAAIFLPLVAMVLLVGGVYFYFSRLQGKSSSLQLPRPRPRPNRITIESAFDNPTYETGSLSFAGDERI

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 928-948

N-glycosylation sites.

amino acids 249-252, 291-294, 315-318, 401-404, 424-427, 438-441, 442-445, 543-546, 585-588, 709-712

N-myristoylation sites.

amino acids 30-35, 34-39, 80-85, 205-210, 209-214, 212-217, 420-425, 437-442, 499-504, 517-522, 542-547, 733-738

Sushi domain (SCR repeat).

amino acids 359-414, 534-591, 712-767, 773-832, 840-897

CUB domains.

amino acids 418-526, 595-703

**FIGURE 152**

MVQKSRNGGVYPGPSGEKKLVGFVGLDPGAPDSTRDGALLIAGSEAPKRGSIILSKPRAGGAGAGKPPKRNAFYRKL  
 QNFLYNVLERPRGWAFIYHAYVFLLVFSCVLVSFSTIKEYEKSSEGALYILEIVTIVVFGVEYFVRIWAAGCCCRY  
 RGWRGRLKFARKPFCVIDIMVLIASIAVLAAGSQGNVFATSALRSLRFLQILRMIRMDRRGGTWKLLGSVVYHSKE  
 LVTAWYIGFLCLILASFVYLAKEGENDHFDTYADALWWGLITLTITIGYGDYQPTWNGRLLAATFTLIGVSFFALP  
 AGILSGSFALKVQEQHRQKHFEKRRNPAAGLIQSAWRFYATNLSRTDLHSTWQYYERTVTVPMYRLIPPLNQLELLR  
 NLKSKSGLAFRKDPPPEPSQKVSLKDRVFSSPRGVAAKKGKSPQAQTVRRSPSADQSLEDSPSKVPKSWFSGDRS  
 RARQAFRIKGAASRQNSEEASLPGEDIVDDKSCPCFVTEDLTPGLKVSIRAVCVMRFLVSKRKFKESLRPYDVM DV  
 IEQYSAGHLDMLSRIKSLQSRVDQIVGRGPAITDKDRTKGPAEELPEDPMMGRLGKVEKQVLSMEKKLDFLVNIY  
 MQRMGIPPTETEAYFGAKEPEPAPPYHSPEDSREHVDRHGCIVKIVRSSSSTGQKNFSAPPAAPPVQCPTSTSWQPQ  
 SHPRQGHGTSPVGDHGSIVRIPPPPAHERSL SAYGGGNRASMEFLRQEDTPGCRPPEGTLRSDTSISIPSDHEEL  
 ERSFSGFSISQSKENLDALNSCYAAVAPCAKVRPYIAEGESDTSDDLCTPCGPPPRSATGEGPFGDVGWAGPRK

Transmembrane domains.

amino acids 89-109, 127-147, 165-185, 184-204, 229-249, 295-315

N-glycosylation sites.

amino acids 350-353, 672-675

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 49-52

Tyrosine kinase phosphorylation site.

amino acids 120-127

N-myristoylation sites.

amino acids 26-31, 30-35, 51-56, 60-65, 61-66, 186-191, 189-194, 310-315, 313-318, 338-343, 428-433, 507-512, 621-626, 729-734, 730-735

Ion transport protein homology.

amino acids 125-312

KCNQ voltage-gated potassium channel homology.

amino acids 417-653

## **FIGURE 153**

MVFAHRMDNSKPHLIIP TLLVPLQNR SCTETATPLPSQYLMELSEEHSWMSNQTDLHYVLKPGEVATASIFFGILWL  
FSIFGNSLVCLVIHRSRRTQSTTNYFVVS MACADLLISVASTPFVLLQFTTGRWTLGSATCKVVRYFQYLTPGVQIY  
VLLSICIDRFYTIVYPLSFKVSREKAKKMIAASWIFDAGFVTPVLFFYGSNWDSHCNYFLPSSWEGTAYTVIHFLVG  
FVIPSVLIIILFYQKVIKYYIWRIGTDGRTVRR TMNIVPRTKVKT IKMFLILNLLFLLSWLPFHVAQLWHPHEQDYKKS  
SLVFTAITWISFSSSASKPTLYSIYNANFRRGMKETFCMSSMKCYRSNAYTIT TSSRMAKKNYVGISEIP SMAKTIT  
KDSIYDSFDREAKEKKLAWPINSNPPNTFV

Transmembrane domains.

amino acids 67-87, 105-125, 147-167, 184-204, 225-245, 273-293, 311-331

N-glycosylation sites.

amino acids 25-28, 52-55

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 306-309

N-myristoylation sites.

amino acids 134-139, 220-225, 340-345

7 transmembrane receptor (rhodopsin family) homology.

amino acids 82-330

**FIGURE 154**

MAVRPGLWPALLGIVLAAWLRGSGAQQSATVANPVPGANPDLLPHFLVEPEDVYIVKNKPVLLVCKAVPATQIFFKC  
 NGEWVRQVDHVIERSTDGSSGLPTMEVRINVSRQQVEKVFGLLEEYWCQCVAWSSSGTTKSQKAYIRIAYLRKNFEQE  
 PLAKEVSLEQGIVLPCRPPGIPPAEVEWLRNEDLVDPSPDNVYITREHSLVVRQARLADTANYTCVAKNIVARRR  
 SASAAVIVYVDGWSWPWSKWSACGLDCTHWSRECSDPAPRNGGEECQGTDLDTNRCTSDLCVHTASGPEDVALYVG  
 LIAVAVCLVLLLLVLILVYCRKKEGLSDVDADSSILTSGFQPVSIKPSKADNPHELLTIQPDLSSTTTTYQGSCLPRQ  
 DGPSPKFQLTNGHLLSPLGGGRHTLHHSSPTSEAEFVSRLSTQNYFRSLPRGTSNMTYGTFFNLGGRLMIPNTGIS  
 LLIPDAIPRGKIYEIYLTLHKPEDVRLPLAGCQTLLSPIVSCGPPGVLLTRPVILAMDHCGEPSPDSSWLRLLKKQS  
 CEGSWEDVLHLGEEAPSHLYYCQLEASACYVFTEQLGRFALVGEALSVAAAKRLKLLLFAPVACTSLEYNIRVYCLH  
 DTHDALKEVVQLEKQLGGQLIQEPRVLHFKDSYHNLRSLIHDVPSLWKSLLVSYQEIPFYHIWNGTQRYLHCTFT  
 LERVSPSTSDLACKLWVWQVEGDGQSFSINFNITKDTRFAELLALESEAGVPALVGPSAFKIPFLIRQKIISSLDPP  
 CRRGADWRTLAQKLHLDShLSFFASKPSPTAMILNLWEARHFPNGNLSQLAAAVAGLGQPDAGLFTVSEAE

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 304-324

N-glycosylation sites.

amino acids 107-110, 218-221, 287-290, 441-444, 682-685, 725-728, 816-819

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 229-232, 536-539

Tyrosine kinase phosphorylation site.

amino acids 212-219

N-myristoylation sites.

amino acids 6-11, 13-18, 24-29, 133-138, 175-180, 255-260, 274-279, 405-410,  
 509-514, 717-722, 828-833

Growth factor and cytokines receptors family signature 2.

amino acids 243-249, 246-252

ZU5 domain.

amino acids 439-542

Death domain.

amino acids 761-841

**FIGURE 155**

MAQALLVPPGPESFRLFTRESLAAIEKRAAEKAKKPKKEQDNDNENKPKNSDLEAGKNLPFIYGDIPPEMVSEPL  
 EDLDPYYINKKTFIVMNKGKAI FRFSATSALYILTPLNPVRKIAIKILVHSLFSMLIMCTILTNCVFM T LSNPPDWT  
 KNVEYTFGTGIYTFESLIKILVRGFCLEDFTFLRDPWNWLD FSVIVMAYVTEFVSLGNVSALRTFRVLRALKTISVIP  
 GLKTIVGALIQSVKKLSVDMILT VFCLSVFALIGLQLFMGNLRNKCLQWPPSDSAFETNTTSYFNGTMDSNGTFVNV  
 TMSTFNWKDNIGDDSHFYVLDGQKDPLLCGNGSDAGQCPEGYICVKAGRNPNGYTSFDTFSWAFSLFLRLMTQDYW  
 ENLYQLTLRAAGKTYTIFVVLVIFLGSFYLVNLI LAVVAMAYEEQNQATLEAEQKEAEFQQMLEQLKKQQEEAAQAV  
 AAASAASRDFSGIGGLGELLESSSEASKLSSKSAKEWRNRRKKRRQREHLEGNNKGERDSFPKSESEDSVKRSSFLF  
 SMDGNRLTSDKKFCSPHQSLLSIRGSLFSPPRRNSKTSIFSFRGRAKDVGSEND FADDEHSTFEDSETRRDSLFEPHR  
 HGERRNSNGTTTETEVRKRRLLSSYQISMEMLEDSSGRQRAVSIA S ILTNTMEELEESRQKCPPCWYRFANVFLIWD  
 CDAWLKVKHLVNLIVMDPFVDLAITICIVLNTLFMAMEHYPMTEQFSSVLT VGNLVFTGIFTAEMVLKIIAMDPYYY  
 FQEGWNI F DGIIVSLSLMELGLSNVEGLSVLRSFRLLRVFKLAKSWPTLNMLIKIIGNSVGALGNLT LVLAIIVFIF  
 AVVGMQLFGKSYKECVCKINDDCTLPRWHMNDFFHSFLIVFRVLCGEWIETMWDCMEVAGQTMCLIVFMLVMVIGNL  
 VVLNLF LALLSSFS SDNLAATDDD NEMNNLQIAVGRMQKGIDYVKNKMRECFQKAFFRKPKVIEIHEGNKIDSCMS  
 NNTGIEISKALNYLRDNGTTS GVG TGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFENLNTEEFSSSESELE  
 ESKEKLNATSSSEGSTVDVVLPREGEQAETEPEEDLKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNLRKTCYSIVE  
 HNWFFETFIVEMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTYI FILEMLLKWVAYGFQTYFTNAWCRLD FLIVD  
 VSLVSLVANALGYSELGAIKSLRTLRLALRPLRLALSRFEGMRVVVNALVGAIPSIMNVLLVCLIFWLIFSIMGVNLFA  
 GKFYHCVNMTTGNMFDISDVNNLSDCQALGKQARWKNVKVNF DNVGAGYLALLQVVS

Transmembrane domains.

amino acids 124-144, 249-269, 402-422, 707-727, 740-760, 778-798, 821-841,  
 837-857, 874-894, 914-934, 1155-1175, 1192-1212, 1224-1244, 1240-1260,  
 1269-1289, 1285-1305

N-glycosylation sites.

amino acids 211-214, 290-293, 296-299, 302-305, 307-310, 339-342, 624-627,  
 835-838, 1002-1005, 1019-1022, 1085-1088, 1317-1320, 1331-1334

Glycosaminoglycan attachment sites.

amino acids 473-476, 1023-1026

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 245-248, 533-536, 570-573, 607-610, 620-623, 635-638

Tyrosine kinase phosphorylation site.

amino acids 1033-1041

N-myristoylation sites.

amino acids 210-215, 271-276, 297-302, 303-308, 340-345, 514-519, 543-548,  
 752-757, 780-785, 827-832, 831-836, 907-912, 1005-1010, 1018-1023, 1020-1025,  
 1024-1029, 1026-1031, 1249-1254, 1281-1286

ATP/GTP-binding site motif A (P-loop).

amino acids 851-858

Ion transport protein.

amino acids 153-423, 742-934, 1190-1365

**FIGURE 156**

MAQALLVPPGPESFRLFTRESLAAIEKRAAEEKAKKPKKEQDNDNENKPKPNSDLEAGKNLPFIYGDIPPEMVSEPL  
 EDLDPYYINKKTFIVMNGKKAIFRSATSALYIITPLNPVRKIAIKILVHSLFSMLIMCTILTNCVFMTLSNPPDWT  
 KNVEYTFGTGIYTFESLIKILARGFCLEDFTLRDPWNWLD FSVIWMAYVTEFVDLGNVSA LRTRFVLRALKTISVIP  
 GLKTI VGALIQSVKKLS DVMILT VFCLSVFALIGLQLFMGNLNRNKCLQWPPSDSAFETNTTSYFNGTMD SNGTFVNV  
 TMSTFNWKDYIGDDSHFYVLDGQKDP LLCNGSDAGQCPEGYICVKAGRNPNGYTSFDTFSWAFSLSLFRLMTQDYW  
 ENLYQLTLRAAGKTYMIF FVLVIFLGSFYLVNLILAVVAMAYEEQNQATLEEA EQKEAEFQQMLEQLKKQOEAAQAV  
 AAASAASRDFSGVGGGLGELLESSSEASKLSSKGAKEWRNRKRQRHLEGNNGKERDSFPKSESEDSVKRSSFLF  
 SMDGNRLTSDKKFCSPHQSLLSIRGSLFSPPRNSKTSIFSFRGRAKDVGSEND FADDEHSTFEDSESRRDSL FVPHR  
 HGERRNSNGTTTETEVKRRLSSYQISMEDLSSGRQRAVSIASILTNTMEELEESRQKPCPCWYRFANVFLIWD C  
 CDAWLKVKHLVNLIVMDPFVDLAITICIVLNTLFMAMEHYPMTEQFSSVLT VGNLVFTGIFTAEMVLKIIAMDPYYY  
 FQEGWNIFDGIIVSLSLMELGLSNVEGLSVLRSLRFLRVFKLAKSWPTLNMLIKIIGNSVGALGNLTLVLAII VFIF  
 AVVGMQLFGKSYKECVCKINDCTLPRWHMNDFFHSLIVFRVLCGEWIE TMWDCEVAGQTMCLIVFMLVMVIGNL  
 VVLNLF LALLLSSFSDDNLAATDDD NEMNNLQIAGVRMOKGIDYVKNKMRECFQKAFFRKPKVIEIHEGNKIDSCMS  
 NNTGIEISKELNYLRDNGTTSVGTGSSVEKYVIDENDYMSFINNPSLTVTVPIAVGESDFENLNTEEFSSSESELE  
 ESKEKLNATSSSEGSTVDVVLPREGEQAETEPEEDFKPEACFTEGCIKKFPFCQVSTEEGKGKIWWNLRKTCYSIVE  
 HNWFFETFIVFMILLSSGALAFEDIYIEQRKTIKTMLEYADKVFTYIFILEMLLKWVAYGFQTYFTNAWCWLDLFDV  
 VSLVSLVANALGYSELGAIKSLRTLRLRPLRALS RFEGMRVVVNALVGAIP SIMNVLLVCLIFWLIFSIMGVNLFA  
 GKPHYCVNMTTGNMFDISDVNNLSDCQALGKQARWKNVKNFNDNVGAGYLALLQVATFKGWMDIMYAAVDSRDVKLQ  
 PVYEENLYMYLYFVIFIIFGSFFTLNLFIGV IIDNFNQKKKFGGQDIFMTEEQKKYYNAMKKLGSKKPKQKPIPRPA  
 NKFQGMVDFVTRQVDFDISIMILICLNMVTMMVETDDQGYMTLVLSRINLVFIVLFTGEFVLKLVSLRHYFTIGW  
 NIFDFVVVILSIVGMFLAEMIEKYSVSP TLFVRILARIGRILRLIKGAKGIRTL LFLALMMSLPALFNIGLLFLVM  
 FIYAIFGMSNFAYVKKEAGIDDMFN FETFGNSMICLFQITTSAGWDGLLAPILNSAPPDCDPDTHPGSSVKGDRGD  
 PSVGIFFFVSYIIISFLVVVNMYIAVILENFSVATEESAEP LSEDDFEMFYEVWEKFDPDATQFIEFSKLSDFAAAL  
 DPPLLIAPKNKVQLIAMDLPMVSGDRIHCLDILFAFTKRVLCESGEMDALRIQMEDRFMASNPSKVSYPEPITTT LKR  
 KQEEVSAAIQRNFRCYLLKQRLKNISSNYNKEAIKGRIDLPIKQDMIIDKLNGNSTPEKTDGSSSTTSPPSYDSVT  
 KPDKEKFEKDKPEKESKGEVRENQK

Transmembrane domains.

amino acids 124-144, 249-269, 402-422, 707-727, 740-760, 778-798, 821-841, 837-857, 874-894, 914-934, 1155-1175, 1191-1211, 1224-1244, 1240-1260, 1269-1289, 1285-1305, 1351-1371, 1396-1416, 1472-1492, 1507-1527, 1538-1558, 1556-1576, 1590-1610, 1606-1626, 1648-1668, 1700-1720

N-glycosylation sites.

amino acids 211-214, 290-293, 296-299, 302-305, 307-310, 339-342, 624-627, 835-838, 1002-1105, 1019-1022, 1085-1088, 1317-1320, 1331-1334, 1724-1727, 1873-1876

Glycosaminoglycan attachment sites.

amino acids 473-476, 1023-1026

Tyrosine kinase phosphorylation sites.

amino acids 1033-1041, 1368-1375

N-myristoylation sites.

amino acids 210-215, 271-276, 297-302, 303-308, 340-345, 514-519, 543-548, 752-757, 780-785, 827-832, 831-836, 907-912, 1005-1010, 1018-1023, 1020-1025, 1024-1029, 1026-1031, 1249-1254, 1281-1286, 1406-1411, 1554-1559, 1911-1916

Cell attachment sequence.

amino acids 1692-1694

ATP/GTP-binding site motif A (P-loop).

amino acids 851-858

Ion transport protein homology

amino acids 153-423, 742-934, 1190-1418, 1508-1721

Calmodulin-binding motif.

amino acids 1852-1872

ATP synthase homology.

amino acids 399-565

ABC-2 type transporter homology.

amino acids 1421-1636

Alg9-like mannosyltransferase family homology.

amino acids 1223-1667



**FIGURE 157**

MGAAAAQAPLGLPAASARLLLLLATSLLLLFAFSLPGSRASNQPPGGGGGTGGDCPGGKGKSINCSSELVRESDVRC  
 DESSCKYGGVCKEDGDGLKACQFQCHTNYIPVCGSNGDTYQNECFLRRAACKHQKEITVIARGPCYSDNGSGSGEG  
 EEEGSGAEVHRKHSKCGPCKYKAECDEDAENVGVCNIDCSGYSFNPVCASDGSSYNNPCFVREASCIKQEQIDIRH  
 LGHCTD TDDTSLLGKKDDGLQYRPDVKDASDQREDVYIGNHMPCPENLNGYCIHGKCEFIYLLRRASCRCESGYTGQ  
 HCEKTD FSILYVVP SRQKLTHVLIAAIIGAVQIAIIVAIVMCITRKCPKNNRGRRQKQNLGHFTSDTSSRMV

Signal sequence.

amino acids 1-39

Transmembrane domain.

amino acids 329-349

N-glycosylation sites.

amino acids 63-66, 147-150

Glycosaminoglycan attachment sites.

amino acids 149-152, 151-154

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 165-168, 295-298

Tyrosine kinase phosphorylation site.

amino acids 246-253

N-myristoylation sites.

amino acids 2-7, 11-16, 36-41, 45-50, 46-51, 47-52, 48-53, 94-99, 148-153,  
 150-155, 187-192, 207-212

Amidation sites.

amino acids 244-247, 360-363

EGF-like domain cysteine pattern signature.

amino acids 299-310

Kazal-type serine protease inhibitor domain.

amino acids 99-143, 190-235

**FIGURE 158**

MLPEQLYFLQSPPEEEPEYHPDASAQELNVRESDVRCDESSCKYGGVCKEDGDGLKCACQFQCHTNYIPVCGSNGD  
 TYQNECFLRRAACKHQKEITVIARGPCYSDNGSGSGEGEEGSGAEVHRKHSKCGPCKYKAECDEDAENVGCVCNID  
 CSGYSFNPVCASDGSSYNNPCFVREASCIKQEQIDIRHLGHCTD TDDTSLLGKKDDGLQYRPDVKDASDQREDVYIG  
 NHMPCPENLNGYCIHGKCEFIYSTQKASCRCESGYTGQHCEKTD FSILYVVPSRQKLTHVLIAAIIGAVQIAIIVAI  
 VMCITRKCPKNNRGRQKQNLGHFTSDTSSRMV

Transmembrane domain.

amino acids 290-310

N-glycosylation site.

amino acids 108-111

Glycosaminoglycan attachment site.

amino acids 110-113, 112-115

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 126-129

Tyrosine kinase phosphorylation site.

amino acids 207-214

N-myristoylation sites.

amino acids 55-60, 109-114, 111-116, 148-153, 168-173

Amidation sites.

amino acids 205-208, 321-324

EGF-like domain cysteine pattern signature.

amino acids 260-271

Kazal-type serine protease inhibitor domains.

amino acids 60-104, 151-196

EGF-like domains.

amino acids 38-64, 236-271